Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.

- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

  http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: December 21, 2005, 12:44:31 ; Search time 54.0459 Seconds
(without alignment)
484.925 Million cell updates/sec

Title: US-09-211-297-39
Perfect score: 1685
Sequence: 1 MRRASRDYTKYLRGSEEMGG.........LLDPDQDATYFGAFKVRDID 317
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1685	100.0	317	2	US-08-996-139-13	Sequence 13, Appl
2	1685	100.0	317	2	US-08-995-659-13	Sequence 13, Appl
3	1685	100.0	317	2	US-09-215-649A-13	Sequence 13, Appl
4	1685	100.0	317	2	US-09-052-521C-4	Sequence 4, Appli
5	1685	100.0	317	2	US-09-577-780-13	Sequence 13, Appl
6	1685	100.0	317	2	US-09-577-800-13	Sequence 13, Appl
7	1685	100.0	317	2	US-09-466-496-13	Sequence 13, Appl
8	1685	100.0	317	2	US-09-871-856-13	Sequence 13, Appl
9	1685	100.0	317	2	US-09-871-291-13	Sequence 13, Appl
10	1685	100.0	317	2	US-09-396-937-2	Sequence 2, Appli
11	1685	100.0	317	2	US-09-877-650-13	Sequence 13, Appl
12	1685	100.0	317	2	US-09-865-363-13	Sequence 13, Appl
13	1685	100.0	317	2	US-09-688-459-13	Sequence 13, Appl
14	1685	100.0	317	2	US-09-957-944-6	Sequence 6, Appli
15	1424.5	84.5	316	2	US-09-957-944-8	Sequence 8, Appli
16	1417.5	84.1	316	1	US-08-842-842-7	Sequence 7, Appli
17	1417.5	84.1	316	2	US-08-989-362-2	Sequence 2, Appli
18	1417.5	84.1	316	2	US-09-052-521C-2	Sequence 2, Appli
19	1417.5	84.1	316	2	US-09-671-658A-2	Sequence 2, Appli
20	1417.5	84.1	316	2	US-09-396-937-4	Sequence 4, Appli
21	1417.5	84.1	316	2	US-09-396-937-6	Sequence 6, Appli
22	1326.5	78.7	294	2	US-08-996-139-11	Sequence 11, Appl
23	1326.5	78.7	294	2	US-08-995-659-11	Sequence 11, Appl
24	1326.5	78.7	294	2	US-09-215-649A-11	Sequence 11, Appl
25	1326.5	78.7	294	2	US-09-577-780-11	Sequence 11, Appl
26	1326.5	78.7	294	2	US-09-577-800-11	Sequence 11, Appl
27	1326.5	78.7	294	2	US-09-466-496-11	Sequence 11, Appl
28	1326.5	78.7	294	2	US-09-871-856-11	Sequence 11, Appl
29	1326.5	78.7	294	2	US-09-871-291-11	Sequence 11, Appl
30	1326.5	78.7	294	2	US-09-877-650-11	Sequence 11, Appl
31	1326.5	78.7	294	2	US-09-865-363-11	Sequence 11, Appl
32	1326.5	78.7	294	2	US-09-688-459-11	Sequence 11, Appl
33	771	45.8	187	2	US-09-396-937-8	Sequence 8, Appl
34	769	45.6	173	2	US-09-396-937-10	Sequence 10, Appl
35	759	45.0	173	2	US-09-396-937-12	Sequence 12, Appl
36	721.5	42.8	188	2	US-09-396-937-14	Sequence 14, Appl
37	711.5	42.2	182	2	US-09-396-937-16	Sequence 16, Appl
38	691	41.0	173	2	US-09-396-937-18	Sequence 18, Appl
39	670	39.8	173	2	US-09-396-937-20	Sequence 20, Appl
40	538	31.9	109	2	US-09-911-777-8	Sequence 8, Appli
41	418	24.8	77	2	US-09-632-287A-11	Sequence 11, Appl
42	418	24.8	77	2	US-10-286-696-11	Sequence 11, Appl
43	363	21.5	77	2	US-09-632-287A-10	Sequence 10, Appl
44	363	21.5	77	2	US-10-286-696-10	Sequence 10, Appl
45	251.5	14.9	279	2	US-09-072-993C-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-996-139-13
; Sequence 13, Application US/0899613
; Patent No. 6017729
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Galibert, Laurent
; APPLICANT: Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,139
; FILING DATE: 22 DECEMBER 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/064,671
; FILING DATE: 14 OCTOBER 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-996-139-13

RESULT 2

US-08-995-659-13

Sequence 13, Application US/08995659

Patent No. 6242213

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Query Match       100.0%;  Score 1685;  DB 2;  Length 317;
Best Local Similarity  100.0%;  Pred. No. 2e-163;  Mismatches 0;
Matches 317;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

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Qy   61  VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK  120

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         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH  180

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Qy  241  YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHPYSINVGGFFKLRSGEEISIEVSNPSLLD  300
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Db  241  YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHPYSINVGGFFKLRSGEEISIEVSNPSLLD  300

Qy  301  PDQDATYFGAFKVRDID  317
         |||||||||||||||||
Db  301  PDQDATYFGAFKVRDID  317
```

GENERAL INFORMATION:

APPLICANT: Anderson, Dirk M.

APPLICANT: Galibert, Laurent

APPLICANT: Maraskovsky, Eugene

TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation, Law Department

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Power Macintosh

OPERATING SYSTEM: Apple Operating System 7.5.5

SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/995,659

FILING DATE: 22 DECEMBER 1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/813,509

FILING DATE: 07 MARCH 1997

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 60/064,671

FILING DATE: 14 OCTOBER 1997

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/772,330

FILING DATE: 23 DECEMBER 1996

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne

REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2852-A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)587-0430

TELEFAX; (206)233-0644

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 317 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-995-659-13

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Query Match       100.0%;  Score 1685;  DB 2;  Length 317;
Best Local Similarity  100.0%;  Pred. No. 2e-163;  Mismatches 0;
Matches 317;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1  MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPPAPHQPPAASRSMFVALLGLGLGQV   60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPPAPHQPPAASRSMFVALLGLGLGQV   60

Qy   61  VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK  120
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Db   61  VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK  120

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Qy  181  KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICPRHHETSGDLATEYLQLMV  240
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Db  241  YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHPYSINVGGFFKLRSGEEISIEVSNPSLLD  300

Qy  301  PDQDATYFGAFKVRDID  317
         |||||||||||||||||
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RESULT 3

US-09-215-649A-13

Sequence 13, Application US/09215649A

Patent No. 6271349

GENERAL INFORMATION:

APPLICANT: Anderson, Dirk M.

Galibert, Laurent

Maraskovsky, Eugene

TITLE OF INVENTION: Receptor Activator of NF-kappaB

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation, Law Department

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Power Macintosh

OPERATING SYSTEM: Apple Operating System 7.5.5

SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/215,649A

FILING DATE: 17-Dec-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/996,139

FILING DATE: <Unknown>

CLASSIFICATION: <Unknown>

APPLICATION NUMBER: USSN 08/813,509

FILING DATE: 07 MARCH 1997

APPLICATION NUMBER: USSN 08/772,330

FILING DATE: 23 DECEMBER 1996

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne

OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: December 21, 2005, 12:35:06 ; Search time 218.262 seconds
(without alignments)
1024.696 Million cell updates/sec

Title: US-09-211-297-39
Perfect score: 1685
Sequence: 1 MRRASRDYTKYLRGSEEMGG.........LLDPDQDATYFGAFKVRDID 317

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	Match DB	ID	Description
1	1685	100.0	317	1	TNF11_HUMAN	O14788 h tumor nec
2	1685	100.0	317	2	Q5T9Y4_HUMAN	Q5t9y4 homo sapien
3	1417.5	84.1	316	1	TNF11_MOUSE	O35235 m tumor nec
4	1396.5	82.9	318	1	TNF11_RAT	Q9ese2 r tumor nec
5	1292	76.7	244	2	Q54A98_HUMAN	Q54a98 homo sapien
6	559.5	33.2	290	2	Q5HZR8_XENLA	Q5hzr8 xenopus lae
7	470	27.9	117	2	Q5XLH0_RABIT	Q5xlh0 oryctolagus
8	273.5	16.2	289	2	Q4VSR6_PIG	Q4vsr6 sus scrofa
9	266	15.8	317	2	Q7ZYX9_BRARE	Q7zyx9 brachydanio
10	265	15.7	304	2	Q7T1F2_CHICK	Q7t1f2 gallus gall
11	262.5	15.6	292	2	Q5ZK93_CHICK	Q5zk93 gallus gall
12	251.5	14.9	281	2	TNF10_HUMAN	P50591 homo sapien
13	251.5	14.9	281	2	Q6IBA9_HUMAN	Q6iba9 homo sapien
14	249.5	14.8	299	2	Q6DHG9_BRARE	Q6dhg9 brachydanio
15	249.5	14.8	303	2	Q5XKN3_MOUSE	Q5xkn3 mus musculu
16	248	14.7	291	2	TNF10_MOUSE	P50592 mus musculu
17	245.5	14.6	264	2	Q4S9Q4_TETNG	Q4s9q4 tetraodon n
18	240.5	14.3	214	2	Q9DDZ5_BRARE	Q9ddz5 brachydanio
19	234	13.9	300	2	Q5U675_HUMAN	Q5u675 homo sapien
20	216.5	12.8	287	2	Q90WT9_CHICK	Q90wt9 gallus gall
21	215.5	12.8	290	2	Q8K3G0_RAT	Q8k3g0 rattus norv
22	211	12.5	285	2	Q4SKU4_TETNG	Q4sku4 tetraodon n
23	200	11.9	282	2	TNFL6_PIG	Q9bea8 sus scrofa
24	194.5	11.5	282	2	Q861W5_FELCA	Q861w5 felis silve
25	190.5	11.3	253	2	Q5CAQ0_CHICK	Q5caq0 gallus gall
26	189	11.2	281	1	TNFL6_HUMAN	P48023 h tumor nec
27	187.5	11.1	279	2	Q53ZZI_HUMAN	Q53zzi homo sapien
28	187.5	11.1	279	2	Q7TMV9_MOUSE	Q7tmv9 mus musculu
29	186	11.0	280	1	TNFL6_MACFA	P63308 m tumor nec
30	186	11.0	280	1	TNFL6_MACMU	P63307 m tumor nec
31	186	11.0	280	1	TNFL6_MACNE	P63306 m tumor nec
32	184.5	10.9	252	2	Q8K3Y8_MOUSE	Q8k3y8 mus musculu
33	184.5	10.9	279	1	TNFL6_MOUSE	P41047 mus musculu
34	184.5	10.9	279	2	Q544E9_MOUSE	Q544e9 mus musculu
35	182.5	10.8	278	2	Q4STX9_TETNG	Q4stx9 tetraodon n
36	182.5	10.8	280	1	TNFL6_CERTO	Q9bdn1 c tumor nec
37	181	10.7	95	2	Q6UWI7_HUMAN	Q6uwi7 homo sapien
38	181	10.7	95	2	Q6UVI3_HUMAN	Q6uvi3 homo sapien
39	179.5	10.7	252	2	Q80Y20_MOUSE	Q80y20 mus musculu
40	177.5	10.5	252	2	Q8K3Y7_RAT	Q8k3y7 rattus norv
41	176.5	10.5	261	1	TNFL5_RAT	P51749 b tumor nec
42	175.5	10.4	278	1	TNFL5_BOVIN	P36940 b tumor nec
43	169.5	10.1	261	1	TNFL5_CALJA	Q9bdn3 c tumor nec
44	167.5	9.9	261	1	TNFL5_AOTTR	Q9bdm3 a tumor nec
45	162	9.6	239	2	Q5OL61_CHICK	Q5ol61 gallus gall

ALIGNMENTS

RESULT 1
TNF11_HUMAN

ID   TNF11_HUMAN   STANDARD;   PRT;   317 AA.
AC   O14788; O14723; Q96Q17; Q9P2Q3;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Tumor necrosis factor ligand superfamily member 11 (Receptor activator
DE   of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-
DE   induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast
DE   differentiation factor) (ODF) [Contains: Tumor necrosis factor ligand
DE   superfamily member 11, membrane form; Tumor necrosis factor ligand
DE   superfamily member 11, soluble form].
GN   Name=TNFSF11; Synonyms=OPGL, RANKL, TRANCE;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE (ISOFORM 1).
RC   TISSUE=Lymph node;
RX   MEDLINE=98032977; PubMed=9367155; DOI=10.1038/36593;
RA   Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
RA   Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
RA   Galibert L.;
RT   "A homologue of the TNF receptor and its ligand enhance T-cell growth
RT   and dendritic-cell function.";
RL   Nature 390:175-179(1997).
RN   [2]
RP   NUCLEOTIDE SEQUENCE (ISOFORM 1).
RC   TISSUE=Bone marrow, and Peripheral blood;
RX   MEDLINE=98227661; PubMed=9568710; DOI=10.1016/S0092-8674(00)81569-X;
RA   Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,
RA   Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,
RA   Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,
RA   Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,
RA   Boyle W.J.;
RT   "Osteoprotegerin ligand is a cytokine that regulates osteoclast
RT   differentiation and activation.";
RL   Cell 93:165-176(1998).
RN   [3]
RP   NUCLEOTIDE SEQUENCE (ISOFORMS 1; 2 AND 3).
RA   Ikeda T., Kuroyama H., Hirokawa K.;
RT   "Determination of human RANKL isoforms.";
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE (ISOFORM 2).
RC   TISSUE=Tongue;
RX   MEDLINE=20175237; PubMed=10708588; DOI=10.1006/bbrc.2000.2314;
RA   Nagai M., Kyakumoto S., Sato N.;
RT   "Cancer cells responsible for humoral hypercalcemia express mRNA
RT   encoding a secreted form of ODF/TRANCE that induces osteoclast
RT   formation.";

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RL   [5]
RL   Biochem. Biophys. Res. Commun. 269:532-536(2000).
RN   [5]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [6]
RP   NUCLEOTIDE SEQUENCE OF 73-317.
RX   MEDLINE=97460112; PubMed=9312123; DOI=10.1074/jbc.272.40.25190;
RA   Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M.,
RA   Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
RA   Choi Y.;
RT   "TRANCE is a novel ligand of the tumor necrosis factor receptor family
RT   that activates c-Jun N-terminal kinase in T cells.";
RL   J. Biol. Chem. 272:25190-25194(1997).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to
CC       TNFRSF11A/RANK. Osteoclast differentiation and activation factor.
CC       Augments the ability of dendritic cells to stimulate naive T-cell
CC       proliferation. May be an important regulator of interactions
CC       between T cells and dendritic cells and may play a role in the
CC       regulation of the T cell-dependent immune response. May also play
CC       an important role in enhanced bone-resorption in humoral
CC       hypercalcemia of malignancy.
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein (isoforms 1 and 3);
CC       Secreted (isoform 2). A soluble form of isoform 1 arises by
CC       proteolytic processing (By similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=3;
CC       Name=1;
CC         IsoId=O14788-1; Sequence=Displayed;
CC       Name=2; Synonyms=SODF;
CC         IsoId=O14788-2; Sequence=VSP_006447;
CC       Name=3;
CC         IsoId=O14788-3; Sequence=VSP_006446;
CC   -!- TISSUE SPECIFICITY: Highest in the peripheral lymph nodes, weak in
CC       spleen, peripheral blood leukocytes, bone marrow, heart, placenta,
CC       skeletal muscle, stomach and thyroid.
CC   -!- INDUCTION: Up-regulated by T cell receptor stimulation.
CC   -!- PTM: The soluble form of isoform 1 derives from the membrane form
CC       by proteolytic processing (By similarity). The cleavage may be
CC       catalyzed by ADAM17.
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   -----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   -----------------------------------------------------------------------
DR   EMBL; AF019047; AAB86811.1; -; mRNA.
DR   EMBL; AF053712; AAC39731.1; -; mRNA.
DR   EMBL; AB064269; BAB79694.1; -; mRNA.
DR   EMBL; AB061227; BAB71768.1; -; mRNA.
DR   EMBL; AB064270; BAB79695.1; -; mRNA.
DR   EMBL; AB037599; BAA90488.1; -; mRNA.
DR   EMBL; BC074823; AAH74823.1; -; mRNA.
DR   EMBL; BC074990; AAH74990.1; -; mRNA.
DR   HSSP; O35235; 1JTZ.
DR   EMBL; AF013171; AAC51762.1; -; mRNA.
DR   SMR; O14788; 162-317.
DR   HGNC; HGNC:11926; TNFSF11.
DR   Ensembl; ENSG00000120659; Homo sapiens.
DR   MIM; 602642; -.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0005887; C:integral to plasma membrane; NAS.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   GO; GO:0030316; P:osteoclast differentiation; NAS.
DR   InterPro; IPR006052; TNF family.
DR   InterPro; IPR006053; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   ProDom; PD002012; TNF subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; FALSE_NEG.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Alternative splicing; Cytokine; Developmental protein;
KW   Differentiation; Glycoprotein; Receptor; Signal-anchor; Transmembrane.
FT   CHAIN         1    317       Tumor necrosis factor ligand superfamily
FT                                member 11, membrane form.
FT   CHAIN       140    317       Tumor necrosis factor ligand superfamily
FT                                member 11, soluble form (By similarity).
FT   TOPO_DOM      1     48       Cytoplasmic (Potential).
FT   TRANSMEM     49     68       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM     69    317       Extracellular (Potential).
FT   SITE        139    140       Cleavage (By similarity).
FT   CARBOHYD    171    171       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD    198    198       N-linked (GlcNAc...) (Potential).
FT   VARSPLIC      1     73       Missing (in isoform 2).
FT                                /FTId=VSP_006446.
FT   VARSPLIC      1     47       Missing (in isoform 3).
FT                                /FTId=VSP_006447.
FT   CONFLICT    194    194       A -> G (in Ref. 6).
SQ   SEQUENCE   317 AA;  35478 MW;  76617646348097F CRC64;

Query Match             100.0%;  Score 1685;  DB 1;  Length 317;
  Best Local Similarity   100.0%;
  Matches  317;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPPAPHQPPAASRSMFVALLGLGLGQV 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy         61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADPQDTTLESQDTKLIPDSCRRIK 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADPQDTTLESQDTKLIPDSCRRIK 120

Qy        121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy        181 KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICRHHETSGDLATEYLQLMV 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICRHHETSGDLATEYLQLMV 240

Qy        241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy        301 PDQDATYFGAFKVRDID 317
              |||||||||||||||||
Db        301 PDQDATYFGAFKVRDID 317

RESULT 2
```

OM protein - protein search, using sw model

```
                    GenCore version 5.1.6
                    Copyright (c) 1993 - 2005 Compugen Ltd.

Run on:           December 21, 2005, 12:34:10 ; Search time 215.664 Seconds
                    (without alignments)
                    645.834 Million cell updates/sec

Title:            US-09-211-297-39
Perfect score:    1685
Sequence:         1 MRRASRDYTKYLRGSEEMGG..........LLDPDQDATYFGAFKVRDID 317
Scoring table:    BLOSUM62
                  Gapop 10.0 , Gapext 0.5
Searched:         2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters:     2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Database :        A_Geneseq_21:*
                  1: geneseqp19808:*
                  2: geneseqp1908:*
                  3: geneseqp20008:*
                  4: geneseqp20018:*
                  5: geneseqp20028:*
                  6: geneseqp20038a:*
                  7: geneseqp2003b8:*
                  8: geneseqp20048:*
                  9: geneseqp20058:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1685	100.0	317	2	AAW83195	Aaw83195 Human ost
2	1685	100.0	317	2	AAW69957	Aaw69957 NF-kB rec
3	1685	100.0	317	2	AAW68293	Aaw68293 NF-kB rec
4	1685	100.0	317	2	AAE08738	Aae08738 Human rec
5	1685	100.0	317	4	AAY84417	Aay84417 Amino aci
6	1685	100.0	317	4	AAE04426	Aae04426 Human rec
7	1685	100.0	317	4	AAE01993	Aae01993 Human ful
8	1685	100.0	317	5	ABB08134	Abb08134 Human RAN
9	1685	100.0	317	5	AAE26103	Aae26103 Human RAN
10	1685	100.0	317	5	ABG31631	Abg31631 Human RAN
11	1685	100.0	317	5	AAU78285	Aau78285 Human TRA
12	1685	100.0	317	5	AAO19096	Aao19096 C neoform
13	1685	100.0	317	5	ADR29336	Adr29336 Human RAN
14	1685	100.0	317	6	ABP55108	Abp55108 Human ost
15	1685	100.0	317	6	AAE34364	Aae34364 Human rec
16	1685	100.0	317	6	ABR42314	Abr42314 Human RAN
17	1685	100.0	317	6	ADB16988	Adb16988 Human rec
18	1685	100.0	317	7	ADC35204	Adc35204 Human TNF
19	1685	100.0	317	7	ADC73002	Adc73002 Human RAN
20	1685	100.0	317	7	ADC78268	Adc78268 Human RAN
21	1685	100.0	317	7	ABW02277	Abw02277 Human RAN
22	1685	100.0	317	7	ADG46723	Adg46723 Human RAN
23	1685	100.0	317	7	ADJ82112	Adj82112 Protein f
24	1685	100.0	317	8	ADM96241	Adm96241 Human rec
25	1685	100.0	317	8	ADT08155	Adt08155 Human RAN
26	1685	100.0	317	8	ADU06570	Adu06570 Novel bro
27	1685	100.0	317	8	ADW09029	Adw09029 Human rec
28	1685	100.0	317	9	ADY16469	Ady16469 PRO polyp
29	1685	100.0	317	9	ADY74714	Ady74714 Human rec
30	1685	100.0	317	9	ADZ12661	Adz12661 Human can
31	1685	100.0	317	9	ADY97756	Ady97756 Human RAN
32	1677	99.5	317	2	AAW83018	Aaw83018 Osteoclas
33	1685	100.0	317	9	ADR29338	Adr29338 Mouse RAN
34	1424.5	84.5	316	8	ADT08153	Adt08153 Murine RA
35	1424.5	84.5	270	7	ADJ82113	Adj82113 Protein f
36	1417.5	84.4	316	2	AAW83017	Aaw83017 Osteoclas
37	1417.5	84.1	316	2	AAW83194	Aaw83194 Human ost
38	1417.5	84.1	316	2	AAW59654	Aaw59654 Amino aci
39	1417.5	84.1	316	2	AAY17874	Aay17874 Murine TR
40	1417.5	84.1	316	3	AAY91024	Aay91024 Mouse OBM
41	1417.5	84.1	316	3	AAY84418	Aay84418 Amino aci
42	1417.5	84.1	316	3	AAY84419	Aay84419 Amino aci
43	1417.5	84.1	316	5	AAU78289	Aau78289 Mouse TRA
44	1417.5	84.1	316	6	ABR42071	Abr42071 Human RAN
45	1417.5	84.1	316	6	ABB99477	Abb99477 Amino aci

ALIGNMENTS

```
RESULT 1
AAW83195
ID   AAW83195 standard; protein; 317 AA.
XX
AC   AAW83195;
XX
DT   11-FEB-1999  (first entry)
XX
DE   Human osteoprotegerin binding protein from the pcDNA/huOPGbp1.1insert.
XX
KW   Human; osteoprotegerin binding protein; OPG binding protein; arthritis;
KW   osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR;
KW   hypercalcaemia; osteoclast differentiation and activation receptor;
KW   Paget's disease.
XX
OS   Homo sapiens.
XX
PN   WO9846751-A1.
XX
PD   22-OCT-1998.
XX
PF   15-APR-1998;  98WO-US007584.
XX
PR   16-APR-1997;  97US-00842842.
PR   23-JUN-1997;  97US-00880855.
PR   30-MAR-1998;  98US-00052521.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Boyle WJ;
XX
DR   WPI; 1998-594578/50.
DR   N-PSDB; AAV70285.
XX
PT   Nucleic acid encoding osteoprotegerin binding protein - useful for, e.g.
PT   treating bone diseases by modulating osteoclast differentiation and for
PT   diagnosis.
XX
PS   Claim 19; Fig 4; 47pp; English.
XX
CC   The present sequence is human osteoprotegerin (OPG) binding protein. Host
CC   cells transfected with vectors containing nucleic acid molecules encoding
CC   OPG binding protein are used to produce recombinant OPG binding protein.
CC   OPG binding protein is used in binding assays to determine osteoprotegerin
CC   (OG) binding protein; to screen for specific binding agents
CC   (OG) in biological samples; to screen for specific binding agents
CC   (particularly agonists and antagonists, including intracellular proteins)
CC   ; to raise Ab (useful in immunoassays for detection of OPG binding
```

CC   protein) and to identify compounds that modulate binding of OPG binding
CC   protein to osteoclast differentiation and activation receptor (ODAR). The
CC   nucleic acid molecule encoding OPG binding protein can be used to detect
XX
CC   OPG binding protein-encoding sequences, e.g. screening for related
CC   sequences, also to produce transgenic animal models, while complementary
CC   sequences are used for antisense regulation of OPG binding protein
CC   expression. Modulators of OPG binding protein, particularly soluble forms
CC   of OPG binding protein or Ab, are used to treat or prevent bone diseases,
CC   e.g. osteoporosis, bone loss caused by arthritis or metastases,
CC   hypercalcaemia, Paget's disease, periodontal disease, osteoporosis,
CC   loosening of prostheses, optionally in combination with agents that
CC   promote bone growth
XX
SQ   Sequence 317 AA;

Query Match   100.0%; Score 1685; DB 2; Length 317;
Best Local Similarity   100.0%; Pred. No. 7.5e-154;
Matches 317; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPPAPHQPPAASRSMFVALLGLGLGQV 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy   61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy   121 QAFQGAVQKELQHIVSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 QAFQGAVQKELQHIVSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy   181 KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240

Qy   241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy   301 PDQDATYFGAFKVRDID 317
          |||||||||||||||||
Db   301 PDQDATYFGAFKVRDID 317

RESULT 2
AAW69957
ID   AAW69957 standard; protein; 317 AA.
XX
AC   AAW69957;
XX
DT   08-OCT-1998 (first entry)
XX
DE   NF-kB receptor activator RANK ligand (RANKL).
XX
KW   RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
KW   immune response; inflammatory response; toxic shock; sepsis; RANKL;
KW   RANK ligand; tumour necrosis factor; TNF.
XX
OS   Homo sapiens.
XX
PN   WO9828426-A2.
XX
PD   02-JUL-1998.
XX
PF   22-DEC-1997; 97WO-US023775.
XX
PR   23-DEC-1996; 96US-0059978P.
PR   07-MAR-1997; 97US-0081350 9.
PR   14-OCT-1997; 97US-0064671P.
XX
PA   (IMMV) IMMUNEX CORP.
XX
PI   Anderson DM, Galibert LJ, Maraskovsky E;

XX
DR   WPI; 1998-377657/32.
DR   N-PSDB; AAV41378.
XX
PT   New isolated ligand for receptor activator of NF-kappa B - used to
PT   develop products for augmenting an immune response for inhibiting an
PT   inflammatory response and for protection of cells.
XX
PS   Claim 27; Page 59-60; 80pp; English.
XX
CC   This represents a human RANKL, a ligand for the RANK (receptor activator
CC   of necrosis factor-kappaB (NF-kB)) polypeptide. RANK is a member of the
CC   tumour necrosis factor (TNF) family. A soluble RANK may be used for
CC   augmenting an immune response. The soluble RANK polypeptide composition
CC   may also be used for regulating an immune or inflammatory response.
CC   Inhibition of NF-kB by RANK antagonists may be useful in ameliorating
CC   negative effects of an inflammatory response that result from triggering
CC   of RANK, e.g. in treating toxic shock or sepsis, graft-versus-host
CC   reactions, or acute inflammatory reactions. They can also be used in
CC   adjunct therapy for disease characterised by neoplastic cells that
CC   express RANK. RANKL polypeptides can also be used to identify inhibitors
CC   of RANK and thus inhibitors of an inflammatory response, and also for
CC   protecting RANK-expressing cells from the negative effects of
CC   chemotherapy or the presence of high levels of TNF-alpha. The products
CC   can also be used for detection and drug screening
XX
SQ   Sequence 317 AA;

Query Match   100.0%; Score 1685; DB 2; Length 317;
Best Local Similarity   100.0%; Pred. No. 7.5e-154;
Matches 317; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPPAPHQPPAASRSMFVALLGLGLGQV 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy   61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy   121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy   181 KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240

Qy   241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy   301 PDQDATYFGAFKVRDID 317
          |||||||||||||||||
Db   301 PDQDATYFGAFKVRDID 317

RESULT 3
AAW68293
ID   AAW68293 standard; protein; 317 AA.
XX
AC   AAW68293;
XX
DT   08-OCT-1998 (first entry)
XX
DE   NF-kB receptor activator RANK ligand (RANKL).
XX
KW   RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
KW   immune response; inflammatory response; toxic shock; sepsis; RANKL;

OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: December 21, 2005, 12:47:51 ; Search time 35.8574 Seconds
(without alignments)
850.612 Million cell updates/sec

Title: US-09-211-297-39
Perfect score: 1685
Sequence: 1 MRRASRDYTKYLRGSEEMGG.........LLDPDQDATYFGAFKVRDID 317

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 9621676J residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 10%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	189	11.2	281	2	I38707	Fas ligand - human
2	184.5	10.9	279	2	A53062	Fas ligand - mouse
3	176.5	10.5	261	2	S53090	CD40 ligand - bovi
4	175.5	10.4	278	2	A49266	fas ligand - rat
5	158.5	9.4	261	2	I53476	CD40 ligand - huma
6	141.5	8.4	235	1	QWMSN	tumor necrosis fac
7	141	8.4	235	1	A25451	tumor necrosis fac
8	137	8.1	234	1	JH0529	tumor necrosis fac
9	133	7.9	233	1	QWHUN	tumor necrosis fac
10	132.5	7.9	233	1	I54490	tumor necrosis fac
11	131.5	7.8	235	2	JU0029	tumor necrosis-beta
12	130.5	7.7	306	2	I49139	lymphotoxin-beta -
13	130	7.7	233	1	S22052	tumor necrosis fac
14	128	7.6	234	1	JQ1344	tumor necrosis fac
15	126.5	7.5	233	1	S24642	tumor necrosis fac
16	126	7.5	232	1	S12606	tumor necrosis fac
17	125.5	7.4	185	2	S52715	tumor necrosis fac
18	122	7.2	193	2	S06192	tumor necrosis fac
19	120	7.1	260	2	S21738	CD40 ligand - mous
20	117	6.9	233	2	S11688	tumor necrosis fac
21	117	6.9	244	2	A46066	lymphotoxin beta
22	97.5	5.8	1464	1	CGHU1S	collagen alpha 1(I
23	94.5	5.6	664	2	C84747	probable protein k
24	92.5	5.5	205	1	QWHUX	hypothetical prote
25	92.5	5.5	450	2	S38114	lymphotoxin alpha
26	91.5	5.4	3848	2	T17414	TipC protein - sli
27	91	5.4	493	2	AC0937	probable GntR-fami
28	90.5	5.4	1694	2	S50065	sialoadhesin - mou
29	90	5.3	730	2	JC1456	gelatinase B (EC 3
30	89.5	5.3	331	2	AF5526	homoprotocatechuat
31	89.5	5.3	379	2	A47659	farnesyl-protein t
32	89	5.3	202	1	B27303	tumor necrosis fac
33	89	5.3	440	2	I49681	glyceraldehyde-3-p
34	89	5.3	479	2	A25052	fibrinogen beta ch
35	89	5.3	639	2	C83624	probable two-compo
36	88.5	5.3	565	2	C89893	hypothetical prote
37	88.5	5.3	578	2	S51379	probable phosphoes
38	88.5	5.3	684	2	T01267	leucine-rich repea
39	88.5	5.3	883	2	A4733	[heparan sulfate] -
40	87.5	5.2	610	2	T06690	galactonolactone d
41	87.5	5.2	1466	1	CGHUTL	collagen alpha 1(I
42	87	5.2	639	2	A32935	protein P1 - Entam
43	87	5.2	1114	2	JH0284	125K surface antig
44	87	5.2	1315	2	G96722	hypothetical prote
45	86.5	5.1	279	2	F72339	hypothetical prote

ALIGNMENTS

RESULT 1
I38707
Fas ligand - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: I38707; JC2340; S57565; I38554
R;Takahashi, T.; Tanaka, M.; Inazawa, J.; Abe, T.; Suda, T.; Nagata, S.
Int. Immunol. 6, 1567-1574, 1994
A;Title: Human Fas ligand: gene structure, chromosomal location and species specificity.
A;Reference number: I38707; MUID:95127560; PMID:7826947
A;Accession: I38707
A;Molecule type: DNA
A;Residues: 1-281 <MIT>
A;Cross-references: UNIPARC:UPI00000D91A; GB:D38122; DDBJ:D29820; NID:g601892; PIDN:BAA
R;Schatzlein, C.E.
submitted to the EMBL Data Library, June 1995
A;Reference number: S57565
A;Accession: S57565
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-281 <RES>
A;Cross-references: UNIPROT:P48023; UNIPARC:UPI00000D91A; EMBL:X89102; NID:g887455; PID:g887456
R;Mita, E.; Hayashi, N.; Iio, S.; Takehara, T.; Hijioka, T.; Kasahara, A.; Fusamoto, H.;
Biochem. Biophys. Res. Commun. 204, 468-474, 1994
A;Title: Role of Fas ligand in apoptosis induced by hepatitis C virus infection.
A;Reference number: JC2340; MUID:95071350; PMID:7980502
A;Accession: JC2340
A;Molecule type: mRNA
A;Residues: 1-281 <SCH>
A;Cross-references: UNIPARC:UPI00000D91A; EMBL:X89102; NID:g887455; PID:g887456
R;Alderson, M.R.; Tough, T.W.; Davis-Smith, T.; Braddy, S.; Falk, B.; Schooley, K.A.; Gr
J. Exp. Med. 181, 71-77, 1995
A;Title: Fas ligand mediates activation-induced cell death in human T lymphocytes.
A;Reference number: I38554; MUID:95105731; PMID:7528780
A;Accession: I38554
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-281 <RE2>
A;Cross-references: UNIPARC:UPI00000D91A; EMBL:U08137; NID:g624627; PIDN:AAC50071.1; PI
A;Gene: FasL
A;Genetic:
A;Introns: 151/1; 116/3
C;Keyword: glycoprotein; transmembrane protein
F;80-102/Domain: transmembrane #status predicted <TMM>
F;76,184,250,260/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match   11.2%;   Score 189;   DB 2;   Length 281;
Best Local Similarity   21.7%;   Pred. No. 2e-08;
Matches   69;   Conservative   43;   Mismatches   98;   Indels   108;   Gaps   11;

Qy   22 PGAPHEGPLHAPPPPAP----HQPPAASRS------------MFVALLGLGLGQVVCS 63

Db 46 PPPPPPPPLPPPPPPPLPPLPLPPLPKRGNHSTGLCLLVMFMVLVALVGLLGIG 100
         |||||| |||||
Qy 64 VALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLLESQDTKLIPDSCRRIKQAF 123
Qy 101 -MFQLFHLQ- 124
         |:|:|
Db 101 -KELAELRESTSQMHTA- 124
Qy 124 QGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLT--INATDIPSGSHK 181
Db 125 -SSLEKQIGH-------------PSPPEKELRKVAHLTGKSNSRSMP----- 159
Qy 182 VSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMVY 241
Db 160 ---LEWEDTYGIVLLSGVKYKKGGLVINETGLYFVYSKVYFRGQSCNN-----LPLSHK 210
Qy 242 VTKTSIKIPSSHTLMKGGSTKY------WSGNSEFHFYSINVGGFFKLRSGEEISIEVSN 295
Db 211 VYMRNSKYPQDLVNMEGKMMSYCTTGQMWARSS------YLGAVFNLTSADHLYVNVSE 263
Qy 296 PSLLDPDQDATYFGAFKV 313
Db 264 LSLVNFEESQTFFGLYKL 281

RESULT 2
A53062
Fas ligand - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: A53062
R;Takahashi, T.; Tanaka, M.; Brannan, C.I.; Jenkins, N.A.; Copeland, N.G.; Suda, T.; Nag
Cell 76, 969-976, 1994
A;Title: Generalized lymphoproliferative disease in mice, caused by a point mutation in
A;Reference number: A53062; MUID:94185175; PMID:7511063
A;Accession: A53062
A;Molecule type: mRNA
A;Status: preliminary
A;Residues: 1-279 <TAK>
A;Cross-references: UNIPROT:P41047; UNIPARC:UPI000000004022; GB:U06948; NID:g473564; PIDN:

Query Match   10.9%; Score 184.5; DB 2; Length 279;
Best Local Similarity 21.7%; Pred. No. 4.9e-08;
Matches 70; Conservative 45; Mismatches 106; Indels 101; Gaps 11;

Qy 13 RGSEEMGGGPGAPHEGPLHAPPPAPHQP-------------------------PAASRSMFVALLGLGL 57
Db 38 RGPDQRRPPPRPPPPVSPLPPPSQPLrPLPTPLPLPKKKDHNTNLWLPVVFFMVLVALVGMGL 97
Qy 58 GQVVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLLESQDTKLIPDSCR 117
Db 98 G---------------------------MYQLFHL------ 105
Qy 118 RIKQAFQGAVQKELQHI--VGSQHIRA---EKAMVDGSWLDLAKRSKLEAQPFAHLTINA 172
Db 106 ---QKELAELREFTNQSLKYSSFEKQIANPS---TPSEKKEPRSVAHLTGN- 150
Qy 173 TDIPSGSHKVSLS-SWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDL 231
Db 151 -----PHSRSIPLEWEDTYGITALISGVKYKKGGLVINETGLYFVYSKVYFRGQSCN-- 201
Qy 232 ATEYLQLMVYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISI 291
Db 202 -NQPLNHKVYMRNS--KYPEDLVIMEEKRLNYCT-TGQIWAHSSYLGAVFNLTSADHLYV 257
Qy 292 EVSNPSLLDPDQDATYFGAFKV 313
Db 258 NISQLSLINFEESKTFFGLYKL 279

RESULT 3
S53090
CD40 ligand - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S53090
R;Mertens, B.E.L.C.; Muriuki, M.
submitted to the EMBL Data Library, February 1995
A;Description: Cloning of bovine CD40L and homology to bovine TNFA and TNFB.
A;Reference number: S53090
A;Accession: S53090
A;Molecule type: mRNA
A;Status: preliminary
A;Residues: 1-261 <MER>
A;Cross-references: UNIPROT:P51749; UNIPARC:UPI0000013709A9; EMBL:Z48469; NID:g732569; PID

Query Match   10.5%; Score 176.5; DB 2; Length 261;
Best Local Similarity 24.2%; Pred. No. 2.1e-07;
Matches 70; Conservative 54; Mismatches 122; Indels 43; Gaps 13;

Qy 33 PPPPAPHQPPAASRSMFVALLGLGL-GQVVCSVALFFYFRAQMDPNRISEDGTHCIYRIL 91
Db 8 PSPRSVATGPPVSMKIFMYLLTVFLITQMIGSALFAVYLHRRLD--KIEDE------R 57
Qy 92 RLHENADFQDT--TLESQDTKLIPDSCRRIKQAFQGAVQKELQHIVGSQHIRAEKAMVDG 149
Db 58 NLHEDPVFMKITQRCNKGEGSLSLLNCEEIRSRFEDLVKDIMQ-----NKEVKKEKNFE- 112
Qy 150 SWLDLAKRSKLEAQPFAHLTINATDIPSGSHKVSLSSWYHDRGWAKISN--MTFSNGK-L 206
Db 113 -----MHGDQEPQIAAHVISEAS------SKTTSVLQW-APKGYYTLSNNLVTLENGKQL 161
Qy 207 IVNQDGFYYLYANICFRHHETSGDLATEYLQLMVYVTKTSIKIP--SSHTLMKGGSTKYW 264
Db 162 AVKRQGFYIYITQVTFCSNR-----ETLSQAPFIASLCLKSPSGSGERILLRAANTH-- 212
Qy 265 SGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLDPDQDATYFGAFKV 313
Db 213 SSSKPCCQQSIHLGGVFELQSGASVFVNVTDPSQVSHGTGFTSFGLLKL 261

RESULT 4
A49266
fas ligand - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: A49266
R;Suda, T.; Takahashi, T.; Golstein, P.; Nagata, S.
Cell 75, 1169-1178, 1993
A;Title: Molecular cloning and expression of the Fas ligand, a novel member of the tumor
A;Reference number: A49266; MUID:94084792; PMID:7505205
A;Accession: A49266
A;Molecule type: mRNA
A;Residues: 1-278 <SUD>
A;Cross-references: UNIPROT:P36940; UNIPARC:UPI000001370B5; GB:U03470; NID:g440178; PIDN:
C;Keywords: glycoprotein; transmembrane protein

Query Match   10.4%; Score 175.5; DB 2; Length 278;
Best Local Similarity 20.3%; Pred. No. 2.8e-07;
Matches 64; Conservative 47; Mismatches 106; Indels 99; Gaps 10;

Qy 21 GPGAPHEGPLHAPPPPAPHQPPAASRSM----------------------FVALLGLGL 57
Db 39 GPGQRPPP--PPPPSPLPPPSQPPLPLPLSPLKKKDNIELWLPVIFFMVLVALVGMGL 96
Qy 58 GQVVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLLESQDTKLIPDSCR 117
Db 97 G--------MYQLFHLQKELAELREFTNHSL--RVSSFEKQIANPSTPSETKKPRSV-- 143
Qy 118 RIKQAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPS 177
Db 144 ---AHLTGNPR--- 151
Qy 178 GSHKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQ 237
Db 152 -SRSIPL-EWEDTYGITALISGVKYKKGGLVINEAGLYFVYSKVYFRGQSCN----SQPLS 205

GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: December 21, 2005, 13:02:07 ; Search time 174.61 Seconds
                           (without alignments)
                           758.559 Million cell updates/sec

Title: US-09-211-297-39
Perfect score: 1685
Sequence: 1 MRRASRDYTKYLRGSEEMGG..........LLDPDQDATYFGAFKVRDID 317

Scoring table: BLOSUM62
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Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                Maximum Match 100%
                Listing first 45 summaries

Database : Published Applications AA_Main:*
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           6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Match Length	DB	ID	Description
1	1685	100.0	317	3	US-09-813-329-7	Sequence 7, Appli
2	1685	100.0	317	3	US-09-871-856-13	Sequence 13, Appl
3	1685	100.0	317	3	US-09-957-944-6	Sequence 6, Appli
4	1685	100.0	317	3	US-09-865-363-13	Sequence 13, Appl
5	1685	100.0	317	3	US-09-871-291-13	Sequence 13, Appl
6	1685	100.0	317	3	US-09-877-650-13	Sequence 13, Appl
7	1685	100.0	317	3	US-09-933-915A-2	Sequence 2, Appli
8	1685	100.0	317	3	US-10-151-071-10	Sequence 10, Appl
9	1685	100.0	317	4	US-10-218-547-22	Sequence 22, Appl
10	1685	100.0	317	4	US-10-405-878-13	Sequence 13, Appl
11	1685	100.0	317	4	US-10-167-182-11	Sequence 11, Appl
12	1685	100.0	317	4	US-10-310-793-28	Sequence 28, Appl
13	1685	100.0	317	4	US-10-460-623-11	Sequence 11, Appl
14	1685	100.0	317	4	US-10-289-456-79	Sequence 79, Appl
15	1685	100.0	317	4	US-10-202-062-22	Sequence 22, Appl
16	1685	100.0	317	4	US-10-664-801-2	Sequence 2, Appli
17	1685	100.0	317	4	US-10-381-160-6	Sequence 6, Appli
18	1685	100.0	317	4	US-10-799-345-12	Sequence 12, Appl
19	1685	100.0	317	5	US-10-399-111-6	Sequence 6, Appli
20	1685	100.0	317	5	US-10-802-133-13	Sequence 13, Appl
21	1685	100.0	317	5	US-10-825-898-4	Sequence 4, Appli
22	1685	100.0	317	5	US-10-854-300-11	Sequence 11, Appl
23	1685	100.0	317	5	US-10-129-595-1	Sequence 1, Appli
24	1685	100.0	317	5	US-10-451-200-6	Sequence 6, Appli
25	1685	100.0	317	5	US-10-999-523-8	Sequence 8, Appli
26	1685	100.0	317	6	US-11-028-780-22	Sequence 22, Appl
27	1685	100.0	317	6	US-11-099-059-6	Sequence 6, Appli
28	1685	100.0	317	6	US-11-135-521-11	Sequence 11, Appl
29	1685	100.0	317	6	US-11-142-736-7	Sequence 7, Appl
30	1424.5	84.5	316	3	US-09-957-944-8	Sequence 8, Appli
31	1424.5	84.5	316	4	US-10-799-345-10	Sequence 10, Appl
32	1424.5	84.5	316	6	US-11-099-059-8	Sequence 8, Appli
33	1422	84.4	270	4	US-10-289-456-80	Sequence 80, Appl
34	1417.5	84.1	316	3	US-09-873-829-4	Sequence 4, Appli
35	1417.5	84.1	316	3	US-09-079-569-7	Sequence 7, Appli
36	1417.5	84.1	316	3	US-09-933-915A-16	Sequence 16, Appl
37	1417.5	84.1	316	4	US-10-017-910-4	Sequence 4, Appli
38	1417.5	84.1	316	4	US-10-105-057-2	Sequence 2, Appli
39	1417.5	84.1	316	4	US-10-272-411-19	Sequence 19, Appl
40	1417.5	84.1	316	4	US-10-326-052-2	Sequence 2, Appli
41	1417.5	84.1	316	4	US-10-272-328A-19	Sequence 19, Appl
42	1417.5	84.1	316	4	US-10-167-182-1	Sequence 1, Appli
43	1417.5	84.1	316	4	US-10-460-623-1	Sequence 1, Appli
44	1417.5	84.1	316	4	US-10-664-801-4	Sequence 4, Appli
45	1417.5	84.1	316	4	US-10-664-801-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-09-813-329-7

; Sequence 7, Application US/09813329
; Patent No. US20020012968A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Suibb Company
; TITLE OF INVENTION: No. US20020012968A1e1 Drosophila Tumor Necrosis Factor Class Mole
; TITLE OF INVENTION: Variants Thereof
; FILE REFERENCE: D0016.np
; CURRENT APPLICATION NUMBER: US/09/813,329
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,816
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 7
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-813-329-7

Query Match   100.0%; Score 1685; DB 3; Length 317;
Best Local Similarity 100.0%; Pred. No. 4.9e-149;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MRRASRDYTKYLRGSEEMGGGGPGAPHEGPLHAPPPPAPHQPPAASRSMFVALLGLGLGQV 60
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Db      1 MRRASRDYTKYLRGSEEMGGGGPGAPHEGPLHAPPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGAVQKELQHIVSSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 QAFQGAVQKELQHIVSSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy    181 KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
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Db    301 PDQDATYFGAFKVRDID 317
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RESULT 2
US-09-871-856-13
Sequence 13, Application US/0987185
Patent No. US20020081720A1
GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
;   Galibert, Laurent
;   MarasKovsKy, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/871,856
; FILING DATE: 31-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/996,139
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-871-856-13

Query Match   100.0%; Score 1685; DB 3; Length 317;
Best Local Similarity   100.0%; Pred. No. 4.9e-149;
Matches 317; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPPAPHQPPAASRSMFVALLGLGLGQV 60
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Qy   61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
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Db 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy 181 KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240

Qy 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
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Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy 301 PPDDATYFGAFKVRDID 317
        |||||||||||||||||
Db 301 PPDDATYFGAFKVRDID 317

RESULT 3
US-09-957-944-6
; Sequence 6, Application US/09957944
; Publication No. US20020063312A1
; GENERAL INFORMATION:
; APPLICANT: Dougall, William C.
; TITLE OF INVENTION: SCREENING ASSAYS FOR AGONISTS AND ANTAGONISTS OF RECEPTOR ACTIVAT...
; TITLE OF INVENTION: NF-kappa B
; FILE REFERENCE: 3109-A
; CURRENT APPLICATION NUMBER: US/09/957,944
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/235,157
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-957-944-6

Query Match   100.0%; Score 1685; DB 3; Length 317;
Best Local Similarity   100.0%; Pred. No. 4.9e-149;
Matches 317; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPPAPHQPPAASRSMFVALLGLGLGQV 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy   61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy 181 KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240

Qy 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy 301 PPDDATYFGAFKVRDID 317
        |||||||||||||||||
Db 301 PPDDATYFGAFKVRDID 317

RESULT 4
US-09-865-363-13
; Sequence 13, Application US/09865363
; Publication No. US20020086826A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
;   Galibert, Laurent
;   MarasKovsKy, Eugene
; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:

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OM protein - protein search, using sw model

                    GenCore version 5.1.6
                    Copyright (c) 1993 - 2005 Compugen Ltd.

Run on:             December 21, 2005, 13:03:52 ; Search time 9.87377 Seconds
                    228.978 Million cell updates/sec

Title:              1685
Perfect score:      US-09-211-297-39
Sequence:           1 MRRASRDYTKYLRGSEEMGG..........LLDPDQDATYFGAFKVRDID 317

Scoring table:      BLOSUM62
                    Gapop 10.0 , Gapext 0.5

Searched:           53982 seqs, 7132107 residues

Total number of hits satisfying chosen parameters:   53982

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Published Applications_AA_New:*
                 1:  /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
                 2:  /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
                 3:  /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
                 4:  /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
                 5:  /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
                 6:  /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
                 7:  /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
                 8:  /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	538	31.9	109	US-11-065-669-8	Sequence 8, Appli
2	251.5	14.9	281	US-10-821-234-1288	Sequence 1288, Ap
3	247.5	14.7	281	US-11-077-272-2	Sequence 2, Appli
4	235.5	14.0	266	US-10-821-234-964	Sequence 964, App
5	232.5	13.8	391	US-11-082-544-10	Sequence 10, Appl
6	147.5	8.8	359	US-11-105-172-4	Sequence 4, Appli
7	134	8.0	240	US-11-105-172-2	Sequence 2, Appli
8	133	7.9	157	US-10-987-663-6	Sequence 6, Appli
9	133	7.9	157	US-11-010-954-1	Sequence 1, Appli
10	133	7.9	157	US-11-053-750-1	Sequence 1, Appli
11	133	7.9	157	US-11-053-749-1	Sequence 1, Appli
12	133	7.9	158	US-11-108-001-12	Sequence 12, Appl
13	133	7.9	164	US-11-082-544-4	Sequence 4, Appli
14	133	7.9	180	US-11-108-001-2	Sequence 2, Appli
15	99.5	5.9	438	US-11-082-544-8	Sequence 8, Appli
16	97.5	5.8	1464	US-10-821-234-1051	Sequence 1051, Ap
17	97	5.8	1464	US-11-186-284-28	Sequence 28, Appl
18	97	5.8	1467	US-11-000-463-243	Sequence 243, App
19	96.5	5.7	371	US-10-821-234-1096	Sequence 1096, Ap
20	92.5	5.5	572	US-10-995-561-572	Sequence 572, App
21	92.5	5.5	177	US-10-999-866-61	Sequence 61, Appl
22	92.5	5.5	1028	US-10-995-561-1028	Sequence 1028, Ap
23	90	5.3	205	US-11-140-417-4	Sequence 4, Appli
24	89	5.3	438	US-11-140-417-2	Sequence 2, Appli
25	88.5	5.3	1163	US-11-044-899-2	Sequence 2, Appli
26	88.5	5.3	1163	US-11-044-899-30	Sequence 30, Appl
27	87.5	5.2	610	US-10-606-302-1	Sequence 1, Appli
28	86.5	5.1	104	US-11-065-669-5	Sequence 5, Appli
29	86.5	5.1	1166	US-10-821-234-964	Sequence 964, App
30	86.5	5.1	1466	US-11-186-284-33	Sequence 33, Appl
31	85	5.0	220	US-11-054-515-3233	Sequence 3233, Ap
32	81.5	4.8	239	US-11-054-515-3232	Sequence 3232, Ap
33	81	4.8	484	US-10-821-234-933	Sequence 933, App
34	79.5	4.7	903	US-11-057-058-65	Sequence 65, Appl
35	79.5	4.7	1001	US-10-467-962B-81	Sequence 81, Appl
36	79	4.7	453	US-10-131-826A-270	Sequence 270, App
37	78.5	4.7	457	US-11-186-284-1185	Sequence 1185, Ap
38	78.5	4.7	400	US-11-054-515-3231	Sequence 3231, Ap
39	77.5	4.6	290	US-11-186-284-155	Sequence 155, App
40	77	4.6	200	US-10-524-198-2	Sequence 2, Appli
41	77	4.6	285	US-11-054-515-3231	Sequence 3231, Ap
42	77	4.6	285	US-10-131-826A-24	Sequence 24, Appli
43	77	4.6	285	US-10-742-634-2	Sequence 2, Appli
44	77	4.6	285	US-11-065-669-1	Sequence 1, Appli
45	76.5	4.5	219	US-11-054-515-3228	Sequence 3228, Ap
				US-11-054-515-3237	Sequence 3237, Ap

ALIGNMENTS

```
RESULT 1
US-11-065-669-8
; Sequence 8, Application US/11065669
; Publication No. US2005024441lA1
; GENERAL INFORMATION:
; APPLICANT: MacKay, Fabienne
; APPLICANT: Kalled, Susan
; TITLE OF INVENTION: BAFF, INHIBITORS THEREOF AND THEIR USE IN THE
; TITLE OF INVENTION: MODULATION OF B-CELL RESPONSE
; FILE REFERENCE: 08201.0024-04000
; CURRENT APPLICATION NUMBER: US/11/065,669
; CURRENT FILING DATE: 2005-02-24
; PRIOR APPLICATION NUMBER: 10/045,574
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 09/911,777
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/143,228
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: PCT/US00/01788
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/117,169
; PRIOR FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 8
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-065-669-8

  Query Match         31.9%;  Score 538;  DB 7;  Length 109;
  Best Local Similarity   75.5%;  Pred. No. 5.9e-44;
  Matches  108;  Conservative   0;  Mismatches   1;  Indels   34;  Gaps   2;

Qy   161 EAQPFAHLTINATDIPSGSHKVSLSSWYHDRGWAKISNMTFSNGKLIVNQGFYYLYANI 220
             ||||||||||||||||||||||||||||||||||||||||||||||| |||
Db     1 EAQPFAHLTINATDIPSGSHKVSLSSWYHDRGWGKISNM----------YANI 43

Qy   221 CFRHHETSGDLATEYLQLMVVVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGF 280
             ||||||||||||||||||||||||||||||||||||||||||| ||||||
Db    44 CFRHHETSGDLATEYLQLMVVVTKTSIKIP----------------SEFHFYSINVGGF 86

Qy   281 FKLRSGEEISIEVSNPSLLDPDQ 303
             |||||||||||||||||||||||
Db    87 FKLRSGEEISIEVSNPSLLDPDQ 109

RESULT 2
```

```
US-10-821-234-1288
; Sequence 1288, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; FILE REFERENCE: 821A
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 1288
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens

Query Match             14.9%;  Score 251.5;  DB 6;  Length 281;
Best Local Similarity   24.1%;  Pred. No. 1.7e-16;
Matches   71;  Conservative  61;  Mismatches 117;  Indels  45;  Gaps  10;

Qy      42 PAASRSMFVALLGLGLGQVVCSVALFFYFRAQMD-------PNRISEDGTHCIYRLRLHENADF 99
           :|| |:       ::  |    |     |:      |    ::|:    |  |  |:
Db      10 PSLGQTCVLIVIFTVLLQSLCVAVTVYVFTNELKQMQDKYSKSGIACF------LKED--- 61

Qy     100 QDTTLESQDTKLIPDSCRRIKQAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSK 159
           :    ::||::  :: :|  |:             ::|: :
Db      62 -DSYWDPNDEESMNSPCWQVKW--------QLRQLVRKMILRTSEETI-----STVQEKQ 107

Qy     160 LEAQPF----------AHLT------INATDIPSGSHKVSL-----SSWYHDR-GWAKISNM 199
           |:::      | :|:|:        :|: |      ||:|:
Db     108 QNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNL 167

Qy     200 TFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMVYVTKTSIKIPSSHTLMKGG 259
            |:| |::: :||||:|:| :| |:::: ::|: |:::|:: : || : |::|::||:|
Db     168 HLRNGELVIHEKGFYYIYSQTYRFQEEIKENTKNDKQMVQYIYKYT-SYPDPILLMKSA 226

Qy     260 STKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLDPDQDATYFGAFKV 313
           ::  | :::|  | ||  ||:|:| ::: | |::|: :: | :: ::|:|||:|
Db     227 RNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLV 280


RESULT 3
US-11-077-272-2
; Sequence 2, Application US/11077272
; Publication No. US20050244927A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, WOON-LAM SUSAN
; APPLICANT: SWARTZ, JAMES R.
; TITLE OF INVENTION: PROCESS FOR PRODUCING POLYPEPTIDES
; FILE REFERENCE: P2019R1
; CURRENT APPLICATION NUMBER: US/11/077,272
; CURRENT FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: US 60/552,678
; PRIOR FILING DATE: 2004-03-11
; NUMBER OF SEQ ID NOS: 7
; SEQ ID NO 2
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens

Query Match             14.7%;  Score 247.5;  DB 7;  Length 281;
Best Local Similarity   24.1%;  Pred. No. 4e-16;
Matches   71;  Conservative  60;  Mismatches 118;  Indels  45;  Gaps  10;

Qy      42 PAASRSMFVALLGLGLGQVVCSVALFFYFRAQMD--PNRISEDGTHCIYRLRLHENADF 99
           :|| |:       ::  |    |     |:      |    ::|:    |  |  |:
```

```
RESULT 4
US-11-082-544-10
; Sequence 10, Application US/11082544
; Publication No. US20050249706A1
; GENERAL INFORMATION:
; APPLICANT: Bermudes, G.
; APPLICANT: King, I.
; APPLICANT: Clairmont, C.
; APPLICANT: Lin, S.
; APPLICANT: Belcourt, M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: TUMOR-TARGETED DELIVERY OF EFFECTOR MOLECULES
; CURRENT APPLICATION NUMBER: US/11/082,544
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: US/09/645,415
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 60/157,581
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: 60/157,637
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion construct

Db      10 PSLGQTCVLIVIFTVLLQSLCVAVTVYVFTNELKQMQDKYSKSGIACF------LKED--- 61
Qy     100 QDTTLESQDTKLIPDSCRRIKQAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSK 159
Db      62 -DSYWDPNDEESMNSPCWQVKW------QLRQLVRKMILRTSEETI-----STVQEKQ 107
Qy     160 LEAQPF----------AHLT------INATDIPSGSHKVSL-----SSWYHDR-GWAKISNM 199
Db     108 QNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNL 167
Qy     200 TFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMVYVTKTSIKIPSSHTLMKGG 259
Db     168 HLRNGELVIHEKGFYYIYSQTYRFQEEIKENTKNDKQMVQYIYKYT-SYPDPILLMKSA 226
Qy     260 STKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLDPDQDATYFGAFKV 313
Db     227 RNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLV 280

Query Match             14.0%;  Score 235.5;  DB 7;  Length 266;
Best Local Similarity   25.3%;  Pred. No. 5e-15;
Matches   65;  Conservative  51;  Mismatches  98;  Indels  43;  Gaps   9;

Qy      77 NRISEDGTHCIYRLRLHENADFQDTTLESQDTKLIPDSCRRIKQAFQGAVQKELQHIVG 136
Db      32 DKYSKSGIACF-----LKED----DSYWDPNDEESMNSPCWQVKW------QLRQLVR 74

Qy     137 SQHIRAEKAMVDGSWLDLAKRSKLEAQPF-------AHLT-----INATDIPSGSHK 181
Db      75 KMILRTSEETI-----STVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNE 129

Qy     182 VSL----SSWYHDR-GWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYL 236
Db     130 KALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYRFQEEIKENTKNDK 189

Qy     237 QLMVYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNP 296
Db     190 QMVQYIYKYT-SYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNE 248

Qy     297 SLLLDPDQDATYFGAFKV 313
Db     249 HLIDMDHEASFGAFLV 265
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OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: December 21, 2005, 12:34:10 ; Search time 169.402 Seconds
(without alignments)
645.834 Million cell updates/sec

Title: US-09-211-297-39_COPY_69_317
Perfect score: 1319
Sequence: 1 YFRAQMDPNRISEDGTHCIY..........LLDPDQDATYFGAPKVRDID 249

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 43937B781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1319	100.0	249	5	ABG94282	Abg94282 Human RAN
2	1319	100.0	249	5	ABG80594	Abg80594 Human rec
3	1319	100.0	249	7	ADJ82115	Adj82115 Protein f
4	1319	100.0	250	6	ADA50079	Adas0079 Human wil
5	1319	100.0	270	7	ADJ82113	Adj82113 Protein f
6	1319	100.0	317	2	AAW83018	Aaw83018 Osteoclas
7	1319	100.0	317	2	AAW83195	Aaw83195 Human ost
8	1319	100.0	317	2	AAW69957	Aaw69957 NF-kB rec
9	1319	100.0	317	2	AAW68293	Aaw68293 NF-kB rec
10	1319	100.0	317	2	AAE08738	Aae08738 Human rec
11	1319	100.0	317	4	AAY84417	Aay84417 Amino aci
12	1319	100.0	317	4	AAE04426	Aae04426 Human rec
13	1319	100.0	317	4	AAE01993	Aae01993 Human ful
14	1319	100.0	317	4	ABB08134	Abb08134 Human RAN
15	1319	100.0	317	5	AAE26103	Aae26103 Human RAN
16	1319	100.0	317	5	ABG31631	Abg31631 Human RAN
17	1319	100.0	317	5	AAU78285	Aau78285 Human TRA
18	1319	100.0	317	5	AAO19096	Aao19096 C neoform
19	1319	100.0	317	5	ADR29336	Adr29336 Human RAN
20	1319	100.0	317	6	ABP55108	Abp55108 Human ost
21	1319	100.0	317	6	AAE34364	Aae34364 Human rec
22	1319	100.0	317	6	ABR42314	Abr42314 Human RAN
23	1319	100.0	317	6	ADB16988	Adb16988 Human RAN
24	1319	100.0	317	7	ADC35204	Adc35204 Human TNF
25	1319	100.0	317	7	ADC73002	Adc73002 Human RAN
26	1319	100.0	317	7	ADC78268	Adc78268 Human RAN
27	1319	100.0	317	7	ABW02277	Abw02277 Human RAN
28	1319	100.0	317	7	ADG46723	Adg46723 Human rec
29	1319	100.0	317	7	ADJ82112	Adj82112 Protein f
30	1319	100.0	317	8	ADM96241	Adm96241 Human rec
31	1319	100.0	317	8	ADT08155	Adt08155 Human RAN
32	1319	100.0	317	8	ADU06570	Adu06570 Novel bro
33	1319	100.0	317	8	ADW09029	Adw09029 Human rec
34	1319	100.0	317	9	ADY74714	Ady74714 Human can
35	1319	100.0	317	9	ADY16469	Ady16469 PRO polyp
36	1319	100.0	317	9	ADY97756	Ady97756 Human RAN
37	1319	100.0	317	9	ADZ12661	Adz12661 Human can
38	1319	99.8	250	6	ADA50095	Adas0095 Human RAN
39	1319	99.8	250	6	ADA50094	Adas0094 Human RAN
40	1316	99.8	250	6	ADA50102	Adas0102 Human RAN
41	1316	99.8	250	6	ADA50098	Adas0098 Human RAN
42	1316	99.7	250	6	ADA50101	Adas0101 Human RAN
43	1315	99.7	250	6	ADA50089	Adas0089 Human RAN
44	1315	99.7	250	6	ADA50086	Adas0086 Human RAN
45	1315	99.7	250	6	ADA50099	Adas0099 Human RAN

ALIGNMENTS

RESULT 1
ABG94282
ID   ABG94282 standard; protein; 249 AA.
XX
AC   ABG94282;
XX
DT   10-DEC-2002 (first entry)
XX
DE   Human RANKL extracellular domain.
XX
KW   Human; mouse; rat; antimicrobial; antiallergic; immunomodulatory;
KW   cytostatic; antiviral; antidiabetic; hypoglycaemic; antigen array;
KW   vaccine; infectious disease.
XX
OS   Homo sapiens.
XX
PN   WO200256905-A2.
XX
PD   25-JUL-2002.
XX
PF   21-JAN-2002; 2002WO-IB000166.
XX
PR   19-JAN-2001; 2001US-0262379P.
PR   04-MAY-2001; 2001US-0285549P.
PR   05-OCT-2001; 2001US-0326998P.
PR   07-NOV-2001; 2001US-0311045P.
XX
PA   (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
PI   Renner WA, Bachmann M, Tissot A, Maurer P, Lechner F, Sebbel P;
PI   Piosek C;
XX
DR   WPI; 2002-627351/67.
XX
PT   Molecular antigen array used in the production of vaccines for infectious
PT   diseases.
XX
PS   Disclosure; Page 420; 441pp; English.
XX
CC   This invention relates to a novel ordered and repetitive antigen array
CC   used in the production of vaccines for infectious diseases. The invention
CC   also discloses a composition comprising a non-natural molecular scaffold
CC   comprising a core particle selected from a core particle of a non-natural
CC   origin and a core particle of natural origin and an organiser comprising
CC   at least one first attachment site, where the organiser is connected to
CC   the core particle by at least one covalent bond. Also disclosed is an
CC   antigen or antigenic determinant with at least one second attachment

```
CC       (Abeta1-42) or its fragment and where the second attachment site is
CC       site, where the antigen or antigenic determinant is amyloid beta peptide
CC       selected from an attachment site not naturally occurring with the antigen
CC       or antigenic determinant and an attachment site naturally occurring with
CC       the antigen or antigenic determinant, where the second attachment site is
CC       capable of association through at least one non-peptide bond to the first
CC       attachment site and where the antigen or antigenic determinant and the
CC       scaffold interact through the association to form an ordered and
CC       repetitive antigen array. The invention also comprises a coat protein
CC       capable of forming a capsid which comprises mutant Qbeta coat proteins
CC       having an amino acid sequence selected from five amino acid sequences
CC       fully defined in the specification. The compounds of the invention may
CC       have antimicrobial, antiallergic, immunomodulatory, cytostatic,
CC       antiviral, antidiabetic, or hypoglycaemic activities and may be used in
CC       immunisation and as a vaccine. The present sequence represents a protein
CC       sequence used to create the compositions of the invention
XX
SQ       Sequence 249 AA;

Query Match      Best Local Similarity   100.0%;    Score 1319;  DB 5;  Length 249;
Matches 249;     Conservative  0;   Pred. No. 9.4e-129;   Indels  0;  Gaps  0;
                 Mismatches  0;

Qy    1 YFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIKQAFQGAVQ 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 YFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIKQAFQGAVQ 60

Qy   61 KELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSHKVSLSSWY 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 KELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSHKVSLSSWY 120

Qy  121 HDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMYVVTKTSIK 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 HDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMYVVTKTSIK 180

Qy  181 IPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLDPDQDATYF 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 IPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLDPDQDATYF 240

Qy  241 GAFKVRDID 249
        |||||||||
Db  241 GAFKVRDID 249

RESULT 2
ABG80594
ID   ABG80594 standard; protein; 249 AA.
XX
AC   ABG80594;
XX
DT   29-NOV-2002  (first entry)
XX
DE   Human receptor activator of NFkB ligand, RANKL, extracellular part.
XX
KW   Molecular antigen array; vaccine; antigen; antimicrobial;
KW   Molecular scaffold; amyloid beta; Abeta 1-42; influenza;
KW   Grave's disease; systemic lupus erythematosus; osteoporosis;
KW   graft versus host disease; IgE-mediated allergic reaction; anaphylaxis;
KW   inflammatory immune disease; myasthenia gravis; multiple sclerosis;
KW   adult respiratory distress syndrome; ARDS; Crohn's disease;
KW   allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;
KW   angioimmunoproliferative lymphadenopathy; immunoblastive lymphoma;
KW   rheumatoid arthritis; diabetes; infectious disease; factor Xa;
KW   enterokinase; cysteine-containing linker.
XX
OS   Homo sapiens.
XX
PN   WO20256907-A2.
XX
PD   25-JUL-2002.
XX
PF   21-JAN-2002; 2002WO-IB000168.
```

```
XX
PR   19-JAN-2001; 2001US-02623797P.
PR   04-MAY-2001; 2001US-0288549P.
PR   05-OCT-2001; 2001US-03269998P.
PR   07-NOV-2001; 2001US-0331045P.
XX
PA   (CYTO-) CYTOS BIOTECHNOLOGY AG.
PA   (NOVS/) NOVARTIS PHARMA AG.
PA   (MAUR/) MAURER P.
PA   (LECH/) LECHNER F.
PA   (ORTM/) ORTMANN R.
PA   (LUEO/) LUEOEND R.
PA   (STAU/) STAUFENBIEL M.
PA   (FREY/) FREY P.
XX
PI   Maurer P, Lechner F, Ortmann R, Lueoend R, Staufenbiel M, Frey P;
PI   Renner WA, Bachmann M, Tissot A, Sebbel P, Piossek C;
XX
DR   WPI; 2002-636514/68.
XX
PT   Molecular antigen array used in the production of vaccines for infectious
PT   diseases.
XX
PS   Disclosure; Page 397; 418pp; English.
XX
CC   The invention relates to a composition comprising: (a) a non-natural
CC   molecular scaffold comprising: (i) a core particle selected from: (1) a
CC   core particle of a non-natural origin; and (2) a core particle of natural
CC   origin; and (ii) an organiser comprising at least one first attachment
CC   site, where the organiser is connected to the core particle by at least
CC   one covalent bond; (b) an antigen or antigenic determinant with at least
CC   one second attachment site, where the antigen or antigenic determinant is
CC   amyloid beta peptide (Abeta 1-42) or its fragment, and where the second
CC   attachment site is selected from: (i) an attachment site not naturally
CC   occurring with the antigen or antigenic determinant; and (ii) an
CC   attachment site naturally occurring with the antigen or antigenic
CC   determinant, where the second attachment site is capable of association
CC   through at least one non-peptide bond to the first attachment site; and
CC   where the antigen or antigenic determinant and the scaffold interact
CC   through the association to form an ordered and repetitive antigen array.
CC   Also included is a process for producing a non-naturally occurring
CC   ordered and repetitive antigen array. The composition is used in
CC   immunisation and as a vaccine for diseases such as influenza, graft
CC   versus host disease, IgE-mediated allergic reactions, anaphylaxis,
CC   respiratory distress syndrome (ARDS), Crohn's disease, allergic asthma,
CC   acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's disease,
CC   systemic lupus erythematosus, inflammatory immune diseases, myasthenia
CC   gravis, immunoproliferative disease lymphadenopathy,
CC   angioimmunoproliferative lymphadenopathy, immunoblastive lymphoma,
CC   rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's disease,
CC   osteoporosis and infectious diseases. The present sequence is modified to
CC   for use in the array of the invention. The antigen is modified to possess
CC   a cleavage site (enterokinase or factor Xa) and a Cysteine- containing N-
CC   or C-terminal linker peptide which serves as the attachment point to a
CC   virus like particle or bacterial protein (the scaffold protein)
XX
SQ   Sequence 249 AA;

Query Match      Best Local Similarity   100.0%;    Score 1319;  DB 5;  Length 249;
Matches 249;     Conservative  0;   Pred. No. 9.4e-129;   Indels  0;  Gaps  0;
                 Mismatches  0;

Qy    1 YFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIKQAFQGAVQ 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 YFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIKQAFQGAVQ 60

Qy   61 KELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSHKVSLSSWY 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 KELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSHKVSLSSWY 120

Qy  121 HDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMYVVTKTSIK 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 HDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMYVVTKTSIK 180
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 21, 2005, 12:47:51 ; Search time 28.1656 Seconds
                                                (without alignments)
                                                850.612 Million cell updates/sec

Title: US-09-211-297-39_COPY_69_317
Perfect score: 1319
Sequence: 1 YFRAQMDPNRISEDGTHCIY.............LLDPDQDATYFGAFKVRDID 249

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR_80:*
               1: pir1:*
               2: pir2:*
               3: pir3:*
               4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	157	11.9	261	2	S53090	CD40 ligand - bovi
2	157	11.9	279	2	A53062	Fas ligand - mouse
3	150	11.4	261	2	S03722	CD40 ligand - mouse
4	149.5	11.3	281	2	I53476	CD40 ligand - huma
5	144	10.9	278	2	I38707	Fas ligand - human
6	141.5	10.7	235	1	A49266	tumor necrosis fac
7	137	10.4	235	1	QWMSN	tumor necrosis fac
8	134.5	10.2	234	1	JH0529	tumor necrosis fac
9	133	10.1	233	1	A25451	tumor necrosis fac
10	132.5	10.1	235	2	QWHUN	tumor necrosis fac
11	132.5	10.0	235	2	I54490	tumor necrosis fac
12	130.5	9.9	306	2	JU0029	tumor necrosis fac
13	130	9.9	233	1	I49139	lymphotoxin-beta -
14	128	9.7	234	1	S22052	lymphotoxin-beta -
15	126.5	9.6	233	1	JQ1344	tumor necrosis fac
16	126	9.6	233	1	S24642	tumor necrosis fac
17	125.5	9.5	185	2	S12606	tumor necrosis fac
18	122	9.2	193	2	S52715	tumor necrosis fac
19	117	8.9	233	2	S06192	tumor necrosis fac
20	117	8.9	244	2	S11688	lymphotoxin beta -
21	102.5	7.8	260	2	A46066	CD40 ligand - mous
22	92.5	7.0	205	1	S21738	lymphotoxin alpha
23	92.5	7.0	450	2	QWHUX	hypothetical prote
24	89	6.7	202	1	S38814	hypothetical prote
25	88.5	6.7	233	2	B27303	tumor necrosis fac
26	88.5	6.7	578	2	C89893	hypothetical prote
27	87	6.6	639	2	S51379	probable phosphoes
28	87	6.6	1114	2	JH0284	125K surface antig
29	86.5	6.6	279	2	F72339	hypothetical prote
30	86	6.5	272	2	AC1090	phage proteins hom
31	85	6.4	1151	2	S03722	DNA-directed DNA p
32	84.5	6.4	197	1	JH0309	tumor necrosis fac
33	84.5	6.4	202	1	JN0869	tumor necrosis fac
34	84	6.4	397	2	G84461	hypothetical prote
35	84	6.4	409	2	G95307	arginine deiminase
36	84	6.4	486	2	C64765	yalf protein precu
37	83.5	6.3	290	2	B97963	conserved hypothet
38	83.5	6.3	399	1	A26916	ribonucleoside-dip
39	83.5	6.3	431	2	F83123	ribonucleoside-dip
40	83.5	6.3	2325	2	T15566	probable porin PA4
41	83	6.3	272	2	AB1454	hypothetical homo
42	83	6.3	333	2	T28466	ribonucleoside-dip
43	83	6.3	479	2	A25052	fibrinogen beta ch
44	83	6.3	3848	2	T17414	fibrinogen - sll
45	82	6.2	160	2	T17005	major allergen Mal

ALIGNMENTS

RESULT 1
S53090
CD40 ligand - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S53090
R;Mertens, B.E.L.C.; Muriuki, M.
submitted to the EMBL Data Library, February 1995
A;Description: Cloning of bovine CD40L and homology to bovine TNFA and TNFB.
A;Reference number: S53090
A;Molecule type: mRNA
A;Status: preliminary
A;Residues: 1-261 <MER>
A;Cross-references: UNIPROT:P51749; UNIPARC:UPI000001370A9; EMBL:Z48469; NID:g732569; PIL

Query Match   11.9%; Score 157; DB 2; Length 261;
Best Local Similarity   25.0%; Pred. No. 2.8e-06;
Matches   57; Conservative 43; Mismatches 96; Indels 32; Gaps 10;

Qy   25 LHENADFQDT--TLESQDTKLIPDSCRRIKQAFQGAVQKELQHIVGSQHIRAEKAMVDGS 82
              |||: || |||::|| |::| |:: ||:||:|: ||:|: ||:|: ||
Db   59 LHEDFVFMKIIQRCNKGEGSLSLLNCEEIRSRFEDLVKDIMQ---NKEVKKEKNFE-- 112

Qy   83 WLDLAKRSKLEAQFPAHLTINATDIPSGSHKVSLSSWYHDRGWAKISN--MTFSNGK-LI 139
              |:| |::| || | |||: :|:: |||: :|| ||||:|::   :||:||| :|
Db   83 ---MHKGDQEPQIAAHVISEAS-----SKTTSVLQW-APKGYYYLSNNLVTLENGKQLA 162

Qy   140 VNQDGFYLYANICRHHETSGDLIATEYLQLMVYTKTSIKIP--SSHTLMKGGSTKYWS 197
              |||||||:| ||:|:||:| || ||||:|::||:|:|| :||||||||||:|::
Db   163 VRKQGFYYIYTQVTFCSNR-----ETLSQAPFIASLCLKSPSGGSERILLRAANTH--S 213

Qy   198 GNSEFHFYSINVGGFFKLRGGEEISTEVSNPSLLDPDQDATYFGAFKV 245
              |:| :|||:| ||||||||:||::|:|::::||::||||||||||:||:
Db   214 SSKPCCQQSIHLGGVFELQSGASVFNVTDPSQVSHGTGFTSFGLLKL 261

RESULT 2
A53062
Fas ligand - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: A53062
R;Takahashi, T.; Tanaka, M.; Brannan, C.I.; Jenkins, N.A.; Copeland, N.G.; Suda, T.; Nag
Cell 76, 969-976, 1994
A;Title: Generalized lymphoproliferative disease in mice, caused by a point mutation in
A;Reference number: A53062; MUID:94185175; PMID:7511063
A;Accession: A53062
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-279 <TAK>
A;Cross-references: UNIPROT:P41047; UNIPARC:UPI000000004022; GB:U06948; NID:g473564; PIDN

RESULT 3
I53476
CD40 ligand - human
N;Alternate names: glycoprotein 39; hCD40-L protein; T-cell antigen gp39; TRAP protein
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: S28017; JH0793; S26694; S28852; I53476; S25684; S30593
R;Hollenbaugh, D.; Grosmaire, L.S.; Kullas, C.D.; Chalupny, N.J.; Braesch-Andersen, S.;
EMBO J. 11, 4313-4321, 1992
A;Title: The human T cell antigen gp39, a member of the TNF gene family, is a ligand for
A;Reference number: S28017; MUID:93049181; PMID:1385114
A;Accession: S28017
A;Molecule type: mRNA
A;Residues: 1-261 <HOL>
A;Cross-references: UNIPROT:P29965; UNIPARC:UPI0000031E7; EMBL:Z15017; NID:g38483; PIDN
R;Spriggs, M.K.; Armitage, R.J.; Strockbine, L.; Clifford, K.N.; Macduff, B.M.; Sato, T.
J. Exp. Med. 176, 1543-1550, 1992
A;Title: Recombinant human CD40 ligand stimulates B cell proliferation and immunoglobuli
A;Reference number: S26694; MUID:93076854; PMID:1280226
A;Accession: S26694
A;Molecule type: mRNA
A;Residues: 1-261 <SPR>
A;Cross-references: UNIPARC:UPI0000031E7; GB:X67878; NID:g38411; PIDN:CAA48077.1; PID:g
A;Experimental source: peripheral blood T-cell
R;Graf, D.; Korthaeuer, U.; Mages, H.W.; Senger, G.; Kroczek, R.A.
Eur. J. Immunol. 22, 3191-3194, 1992
A;Title: Cloning of TRAP, a ligand for CD40 on human T cells.
A;Reference number: S26694; MUID:93076854; PMID:1280226
A;Accession: S26694
A;Molecule type: mRNA
A;Residues: 1-261 <GRA>
A;Cross-references: UNIPARC:UPI0000031E7; EMBL:L07414; NID:g180123; PIDN:AAA35662.1; PI
A;Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 in having 6-Gln
R;Gauchat, J.F.; Aubry, J.P.; Mazzei, G.; Life, P.; Jomotte, T.; Elson, G.; Bonnefoy, J.
FEBS Lett. 315, 259-266, 1993
A;Title: Human CD40-ligand: molecular cloning, cellular distribution and regulation of e
A;Reference number: S28852; MUID:93118085; PMID:7678552
A;Accession: S28852
A;Molecule type: mRNA
A;Residues: 1-261 <GAU>
A;Cross-references: UNIPARC:UPI0000031E7; EMBL:L07414; NID:g180123; PIDN:AAA35662.1; PI
A;Gene: GDB:CD40LG; HIGM1; IMD3
C;Genetics:
A;Cross-references: GDB:120632; OMIM:308230
A;Map position: Xq26-Xq26
C;Keywords: glycoprotein; transmembrane protein
A;Gene: GDB:CD40LG
A;Cross-references: transmembrane #status predicted <TMM>
F;13-44/Domain: transmembrane #status predicted <TMM>
F;45-261/Domain: extracellular #status predicted <EXT>
F;6,240/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match   11.9%; Score 157; DB 2; Length 279;
Best Local Similarity 25.9%; Pred. No. 3e-06;
Matches 50; Conservative 38; Mismatches 81; Indels 24; Gaps   8;

```
Qy   59 VQKELQHI--VGSQHIRA---EKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSHK 113
                           | | |  |  | |  ||     | | | | |   |
Db  105 LQKELAELREFTNQSLKVSSFEKQIANPS----TPSEKKEPRSVAHLTGN------PHS 153

Qy  114 VSLS-SWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 172
         | |   ||| | || |     ||| ||| | |||  ||  || ||||| |  |
Db  154 RSTPLEWEDTYGTALISGVKYKKGGLVINETGLYFVVSKVYFRGQSCN----NQPLNHKV 209

Qy  173 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINGGFFKLRSGEEISIEVSNPSLLD 232
         | | |  |  ||||||||| |  |||||||||||| ||||||  |||||||||  |
Db  210 YMRNS--KYPEDLVLMEEKRLNYCT-TGQIWAHSSYLGAVFNLTSADHLYVNISQLSLIN 266

Qy  233 PQDDATYFGAFKV 245
         | ||||||||||
Db  267 FEESKTFGLYKL 279
```

RESULT 4
I38707
Fas ligand - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: I38707; JC2340; S57565; I38554
R;Takahashi, T.; Tanaka, M.; Inazawa, J.; Abe, T.; Suda, T.; Nagata, S.
Int. Immunol. 6, 1567-1574, 1994
A;Title: Human Fas ligand: gene structure, chromosomal location and species specificity.
A;Reference number: I38707; MUID:95127560; PMID:7826947
A;Accession: I38707
A;Molecule type: DNA
A;Residues: 1-281 <MIT>
A;Cross-references: UNIPARC:UPI000000D91A; GB:D38122; DDBJ:D29820; NID:g601892; PIDN:BAA
R;Schatzlein, C.E.
submitted to the EMBL Data Library, June 1995
A;Reference number: S57565
A;Accession: S57565
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-281 <SCH>
A;Cross-references: UNIPARC:UPI000000D91A; EMBL:X91102; NID:g887455; PID:g887456
R;Alderson, M.R.; Tough, T.W.; Davis-Smith, T.; Braddy, S.; Falk, B.; Schooley, K.A.; Go
J. Exp. Med. 181, 71-77, 1995
A;Title: Fas ligand mediates activation-induced cell death in human T lymphocytes.
A;Reference number: I38554; MUID:95105731; PMID:7528780
A;Accession: I38554
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-281 <RE2>
A;Cross-references: UNIPARC:UPI000000D91A; EMBL:U08137; NID:g624627; PIDN:AAC50071.1; PI
A;Gene: FasL
C;Genetics:
A;Introns: 151/1; 116/3
C;Keywords: glycoprotein; transmembrane protein
F;80-102/Domain: transmembrane #status predicted <TMM>
F;76,184,250,260/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match   11.4%; Score 150; DB 2; Length 261;
Best Local Similarity 25.4%; Pred. No. 1.1e-05;
Matches 58; Conservative 43; Mismatches 95; Indels 32; Gaps 12;

```
Qy   25 LHENADFQDT--TLESQDTKLIPDSCRRIKQAFQGAVQKELQHIVGSQHIRAEKAMVDGS 82
            |  | ||    |  | | |     |  |  |  |||  |  |  | ||
Db   59 LHEDFVFMKTIQRCNTGERSLSLLNCEEIKSQPEGFV-KDIM------LNKEETKEENS 110

Qy   83 WLDLAKRSKLEAQPFAHLTINATDIPSGSHKVSLSSWYHDRGWAKISN--MTFSNGK-LI 139
         ||||||||||||||||||| | ||||||| |  |||||  | || |    |||| | |
Db  111 F-EMQKGDQ-NPQIAAHVISEAS-----SKTTSVLQW-AEKGYYTMSNNLVTLENGKQLT 162

Qy  140 VNQDGFYYLYANICFRHHETSGDLATEYLQLMVYVTKTSIKIPS--SHTLMKGGSTKYWS 197
         |||||||||||||||||||||||||||||  | | |||||||    ||||||||||| |
Db  163 VKRQGLYYIYAQVTFCSNREASSQAP------FIASLCLKSPGRFERILLRAANTH--S 213

Qy  198 GNSEFHFYSINGGFFKLRSGEEISIEVSNPSLLDDPQDDATYFGAFKV 245
         |||||||||||||||||||||||||||||||||  | ||||||||||
Db  214 SAKPCGQQSIHLGGVFELQPGASVFVNVTDPSQVSHGTFTSFGLLKL 261
```

RESULT 5
Query Match   11.3%; Score 149.5; DB 2; Length 281;
Best Local Similarity 23.9%; Pred. No. 1.4e-05;
Matches 47; Conservative 33; Mismatches 74; Indels 43; Gaps   6;

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Qy   59 VQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQ---------------------PFAHLT--INATDIPSGSHK 113
            | | |   ||  |  |    |  |||||||||||
Db   71 HIRAEKAMVDGSWLDLAKRSKLEAQ--------------------------PFAHLT--INATDIPSGSHKV 114
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OM protein - protein search, using sw model

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Run on: December 21, 2005, 12:35:06 ; Search time 171.443 Seconds
(without alignments)
1024.696 Million cell updates/sec

Title: US-09-211-297-39_COPY_69_317
Perfect score: 1319
Sequence: 1 YFRAQMDPNRISEDGTHCIY.........LLDPDQDATYFGAFKVRDID 249

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   UniProt_05.80:*
                1: uniprot_sprot:*
                2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1319	100.0	317	1	TNF11_HUMAN	O14788 h tumor nec
2	1319	100.0	317	2	Q5TY4_HUMAN	Q5ty4 homo sapien
3	1292	98.0	244	2	Q54A98_HUMAN	Q54a98 homo sapien
4	1127	85.4	316	1	TNF11_MOUSE	O35235 m tumor nec
5	1118	84.8	318	1	TNF11_RAT	Q9ee2 r tumor nec
6	482	36.5	290	2	Q5HZR8_XENLA	Q5hzr8 xenopus lae
7	470	35.6	117	2	Q5XLH0_RABIT	Q5xlh0 oryctolagus
8	253.5	19.2	317	2	Q7ZYX9_BRARE	Q7zyx9 brachydanio
9	252.5	19.1	317	2	Q4VSR6_PIG	Q4vsr6 sus scrofa
10	242	18.3	304	2	Q7T1F2_CHICK	Q7t1f2 gallus gall
11	241.5	18.3	303	2	Q5XKN3_MOUSE	Q5xkn3 mus musculu
12	240.5	18.2	214	2	Q9DDZ5_BRARE	Q9ddz5 brachydanio
13	239.5	18.2	292	2	Q5ZK93_CHICK	Q5zk93 gallus gall
14	238.5	18.1	291	1	TNF10_MOUSE	P50592 mus musculu
15	238	18.1	291	2	Q4S9Q4_TETNG	Q4s9q4 tetraodon n
16	237	18.0	299	2	Q6DHG9_BRARE	Q6dhg9 brachydanio
17	236.5	17.9	281	1	P50591_HUMAN	P50591 homo sapien
18	236.5	17.9	281	2	Q6IBA9_HUMAN	Q6iba9 homo sapien
19	219	16.6	300	2	Q5U675_HUMAN	Q5u675 homo sapien
20	216.5	16.4	287	2	Q90WT9_CHICK	Q90wt9 gallus gall
21	211	16.0	285	2	Q4SKU4_TETNG	Q4sku4 tetraodon n
22	207.5	15.7	287	2	Q8K3G0_RAT	Q8k3g0 rattus norv
23	184.5	14.0	252	2	Q8K3Y8_MOUSE	Q8k3y8 mus musculu
24	181	13.7	95	2	Q6UWL7_HUMAN	Q6uwl7 homo sapien
25	181	13.7	95	2	Q6UY13_HUMAN	Q6uy13 homo sapien
26	179.5	13.6	252	2	Q80YZ0_MOUSE	Q80yz0 mus musculu
27	177.5	13.5	253	2	Q8K3Y7_RAT	Q8k3y7 rattus norv
28	172.5	13.1	253	2	Q5CAQ0_CHICK	Q5caq0 gallus gall
29	171	13.0	278	2	Q4STX9_TETNG	Q4stx9 tetraodon n
30	162	12.3	239	2	Q50L61_CHICK	Q50l61 gallus gall
31	160	12.1	207	2	Q58G74_CHICK	Q58g74 gallus gall
32	160	12.1	279	2	Q7TMV9_MOUSE	Q7tmv9 mus musculu
33	158	12.0	98	2	Q4T6H7_TETNG	Q4t6h7 tetraodon n
34	157.5	11.9	282	1	Q9BEA8_PIG	Q9bea8 sus scrofa
35	157	11.9	261	1	TNFL6_BOVIN	P51749 b tumor nec
36	157	11.9	279	1	TNFL6_MOUSE	P41047 mus musculu
37	157	11.9	279	1	Q54E9_MOUSE	Q54e9 mus musculu
38	156.5	11.9	192	2	Q5VJK8_HUMAN	Q5vjk8 homo sapien
39	156.5	11.9	251	2	Q8NFE9_HUMAN	Q8nfe9 homo sapien
40	155	11.8	280	2	Q861W5_FELCA	Q861w5 felis silve
41	150	11.4	261	1	TNFL5_CALJA	Q9bdm3 a tumor nec
42	150	11.4	261	1	TNFL5_AOTTR	Q9bdn3 c tumor nec
43	149.5	11.3	280	1	TNFL5_HUMAN	P29965 h tumor nec
44	149.5	11.3	280	1	TNFL5_MACFA	P63308 m tumor nec
45	149.5	11.3	280	1	TNFL5_MACMU	P63307 m tumor nec

ALIGNMENTS

RESULT 1
TNF11_HUMAN

```
ID   TNF11_HUMAN     STANDARD;     PRT;     317 AA.
AC   O14788; O14723; Q96Q17; Q9P2Q3;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Tumor necrosis factor ligand superfamily member 11 (Receptor activator
DE   of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-
DE   induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast
DE   differentiation factor) (ODF) [Contains: Tumor necrosis factor ligand
DE   superfamily member 11, membrane form; Tumor necrosis factor ligand
DE   superfamily member 11, soluble form].
GN   Name=TNFSF11; Synonyms=OPGL, RANKL, TRANCE;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE (ISOFORM 1).
RC   TISSUE=Bone marrow, and Peripheral blood;
RX   MEDLINE=98032977; PubMed=9367155; DOI=10.1038/36593;
RA   Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
RA   Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
RA   Galibert L.;
RT   "A homologue of the TNF receptor and its ligand enhance T-cell growth
RT   and dendritic-cell function.";
RL   Nature 390:175-179(1997).
RN   [2]
RP   NUCLEOTIDE SEQUENCE (ISOFORM 1).
RC   TISSUE=Lymph node;
RX   MEDLINE=98327661; PubMed=9568710; DOI=10.1016/S0092-8674(00)81569-X;
RA   Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,
RA   Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,
RA   Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,
RA   Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,
RA   Boyle W.J.;
RT   "Osteoprotegerin ligand is a cytokine that regulates osteoclast
RT   differentiation and activation.";
RL   Cell 93:165-176(1998).
RN   [3]
RP   NUCLEOTIDE SEQUENCE (ISOFORMS 1; 2 AND 3).
RA   Ikeda T., Kuroyama H., Hirokawa K.;
RT   "Determination of human RANKL isoforms.";
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE (ISOFORM 2).
RC   TISSUE=Tongue;
RX   MEDLINE=20175237; PubMed=10708588; DOI=10.1006/bbrc.2000.2314;
RA   Nagai M., Kyakumoto S., Sato N.;
RT   "Cancer cells responsible for humoral hypercalcemia express mRNA
RT   encoding a secreted form of ODF/TRANCE that induces osteoclast
RT   formation.";
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RL   Biochem. Biophys. Res. Commun. 269:532-536(2000).
RN   [5]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [6]
RP   NUCLEOTIDE SEQUENCE OF 73-317.
RC   TISSUE=Thymocyte;
RX   MEDLINE=97460112; PubMed=9312132; DOI=10.1074/jbc.272.40.25190;
RA   Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M.,
RA   Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
RA   Choi Y.;
RT   "TRANCE is a novel ligand of the tumor necrosis factor receptor family
RT   that activates c-Jun N-terminal kinase in T cells.";
RL   J. Biol. Chem. 272:25190-25194(1997).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to
CC       TNFRSF11A/RANK. Osteoclast differentiation and activation factor.
CC       Augments the ability of dendritic cells to stimulate naive T-cell
CC       proliferation. May be an important regulator of interactions
CC       between T cells and dendritic cells and may play a role in the
CC       regulation of the T cell-dependent immune response. May also play
CC       an important role in enhanced bone-resorption in humoral
CC       hypercalcemia of malignancy.
CC   -!- SUBUNIT: Homotrimer. (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein (isoforms 1 and 3);
CC       Secreted (isoform 2). A soluble form of isoform 1 arises by
CC       proteolytic processing (By similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=3;
CC       Name=1;
CC         IsoId=O14788-1; Sequence=Displayed;
CC       Name=2; Synonyms=SODF;
CC         IsoId=O14788-2; Sequence=VSP_006447;
CC       Name=3;
CC         IsoId=O14788-3; Sequence=VSP_006446;
CC   -!- TISSUE SPECIFICITY: Highest in the peripheral lymph nodes, weak in
CC       spleen, peripheral blood leukocytes, bone marrow, heart, placenta,
CC       skeletal muscle, stomach and thyroid.
CC   -!- INDUCTION: Up-regulated by T cell receptor stimulation.
CC   -!- PTM: The soluble form of isoform 1 derives from the membrane form
CC       by proteolytic processing (By similarity). The cleavage may be
CC       catalyzed by ADAM17.
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   -----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   -----------------------------------------------------------------------
DR   EMBL; AF019047; AAB86811.1; -; mRNA.
DR   EMBL; AF053712; AAC39731.1; -; mRNA.
DR   EMBL; AB064269; BAB79694.1; -; mRNA.
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DR   EMBL; AB061227; BAB71768.1; -; mRNA.
DR   EMBL; AB064270; BAB79695.1; -; mRNA.
DR   EMBL; AB037599; BAA90488.1; -; mRNA.
DR   EMBL; BC074823; AAH74823.1; -; mRNA.
DR   EMBL; BC074890; AAH74890.1; -; mRNA.
DR   EMBL; AF013171; AAC51762.1; -; mRNA.
DR   HSSP; O35235; 1JTZ.
DR   SMR; O14788; 162-317.
DR   Ensembl; ENSG00000120659; Homo sapiens.
DR   HGNC; HGNC:11926; TNFSF11.
DR   MIM; 602642; -.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0005887; C:integral to plasma membrane; NAS.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   GO; GO:0030316; P:osteoclast differentiation; NAS.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; FALSE_NEG.
DR   PROSITE; PS00049; TNF_2; 1.
DR   PROSITE; PS50049; TNF; 1.
KW   Alternative splicing; Glycoprotein; Receptor; Signal-anchor; Transmembrane.
KW   Differentiation; Cytokine; Developmental protein;
FT   CHAIN       140    317       Tumor necrosis factor ligand superfamily
FT                                member 11, soluble form.
FT   CHAIN         1    317       Tumor necrosis factor ligand superfamily
FT                                member 11, membrane form.
FT   TOPO_DOM      1     47       Cytoplasmic (Potential).
FT   TRANSMEM     48     68       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM     69    317       Extracellular (Potential).
FT   SITE        139    140       Cleavage (By similarity).
FT   CARBOHYD    171    171       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD    198    198       N-linked (GlcNAc...) (Potential).
FT   VARSPLIC      1     73       Missing (in isoform 2).
FT                                /FTId=VSP_006447.
FT   VARSPLIC      1     47       Missing (In isoform 3).
FT                                /FTId=VSP_006446.
FT   CONFLICT    194    194       A -> G (in Ref. 6).
SQ   SEQUENCE   317 AA;  35478 MW;  76617646348097F CRC64;

Query Match             100.0%;  Score 1319;  DB 1;  Length 317;
Best Local Similarity   100.0%;  Pred. No. 4e-110;
Matches  249;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

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Qy     61 KELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSHKVSLSSWY 120
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Qy    121 HDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMVVTKTSIK 180
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Db    189 HDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMVVTKTSIK 248

Qy    181 IPSSHTLMKGGSTKYWSGNSEHFYSINVGGFFKLRSGEEISIEVSNPSLLDPDQDATYF 240
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AC   Q5T9Y4;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
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OM protein - protein search, using sw model

GenCore version 5.1.6
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Run on: December 21, 2005, 12:44:31 ; Search time 42.4525 Seconds
                 484.925 Million cell updates/sec

Title: US-09-211-297-39_COPY_69_317
Perfect score: 1319
Sequence: 1 YFRAQMDPNRISEDGTHCIY.........LLDPDQDATYFGAFKVRDID 249

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_AA:*
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          2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
          3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
          4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
          5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
          6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1319	100.0	317	2	US-08-996-139-13	Sequence 13, Appl
2	1319	100.0	317	2	US-08-995-659-13	Sequence 13, Appl
3	1319	100.0	317	2	US-09-215-649A-13	Sequence 13, Appli
4	1319	100.0	317	2	US-09-052-521C-4	Sequence 4, Appli
5	1319	100.0	317	2	US-09-577-780-13	Sequence 13, Appl
6	1319	100.0	317	2	US-09-577-800-13	Sequence 13, Appl
7	1319	100.0	317	2	US-09-466-496-13	Sequence 13, Appl
8	1319	100.0	317	2	US-09-871-856-13	Sequence 13, Appl
9	1319	100.0	317	2	US-09-871-291-13	Sequence 13, Appl
10	1319	100.0	317	2	US-09-396-937-2	Sequence 2, Appli
11	1319	100.0	317	2	US-09-877-650-13	Sequence 13, Appl
12	1319	100.0	317	2	US-09-865-363-13	Sequence 13, Appl
13	1319	100.0	317	2	US-09-688-459-13	Sequence 13, Appl
14	1319	100.0	317	2	US-09-957-944-6	Sequence 6, Appli
15	1134	86.0	294	2	US-09-215-649A-11	Sequence 11, Appl
16	1134	86.0	294	2	US-08-995-659-11	Sequence 11, Appl
17	1134	86.0	294	2	US-09-577-780-11	Sequence 11, Appl
18	1134	86.0	294	2	US-08-996-139-11	Sequence 11, Appl
19	1134	86.0	294	2	US-09-577-800-11	Sequence 11, Appl
20	1134	86.0	294	2	US-09-466-496-11	Sequence 11, Appl
21	1134	86.0	294	2	US-09-871-856-11	Sequence 11, Appl
22	1134	86.0	294	2	US-09-877-291-11	Sequence 11, Appl
23	1134	86.0	294	2	US-09-865-363-11	Sequence 11, Appl
24	1134	86.0	294	2	US-09-877-650-11	Sequence 11, Appl
25	1134	86.0	294	2	US-09-688-459-11	Sequence 11, Appl
26	1134	86.0	294	2	US-09-957-944-8	Sequence 8, Appli
27	1127	85.4	316	1	US-08-842-842-7	Sequence 7, Appli
28	1127	85.4	316	2	US-08-670-354-6	Sequence 6, Appli
29	1127	85.4	316	2	US-08-989-362-2	Sequence 2, Appli
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31	1127	85.4	316	2	US-09-671-658A-2	Sequence 2, Appli
32	1127	85.4	316	2	US-09-396-937-4	Sequence 4, Appli
33	771	58.5	187	2	US-09-396-937-6	Sequence 6, Appli
34	769	58.3	173	2	US-09-396-937-8	Sequence 8, Appli
35	759	57.5	173	2	US-09-396-937-10	Sequence 10, Appl
36	721.5	54.7	188	2	US-09-396-937-12	Sequence 12, Appl
37	711.5	53.9	182	2	US-09-396-937-14	Sequence 14, Appl
38	691	52.4	173	2	US-09-396-937-16	Sequence 16, Appl
39	670	50.8	173	2	US-09-396-937-18	Sequence 18, Appl
40	538	40.8	109	2	US-09-396-937-20	Sequence 20, Appl
41	418	31.7	77	2	US-09-911-777-8	Sequence 8, Appli
42	418	31.7	77	2	US-09-632-287A-11	Sequence 11, Appl
43	363	27.5	77	2	US-10-286-696-11	Sequence 11, Appl
44	363	27.5	77	2	US-09-632-287A-10	Sequence 10, Appl
45	238.5	18.1	291	1	US-10-286-696-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-08-996-139-13
; Sequence 13, Application US/0899613 9
; Patent No. 6017729
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Galibert, Laurent
; APPLICANT: Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,139
; FILING DATE: 22 DECEMBER 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/064,671
; FILING DATE: 14 OCTOBER 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-996-139-13

Query Match
Best Local Similarity   100.0%;   Score 1319;   DB 2;   Length 317;
Matches 249; Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Qy  121  HDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMYYVTKTSIK  180
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Qy  181  IPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLDPDQDATYF  240
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Db  249  IPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLDPDQDATYF  308

Qy  241  GAFKVRDID  249
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Db  309  GAFKVRDID  317
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RESULT 2
US-08-995-659-13
; Sequence 13, Application US/0895659
; Patent No. 6242213
GENERAL INFORMATION:
  APPLICANT: Anderson, Dirk M.
  APPLICANT: Galibert, Laurent
  APPLICANT: Maraskovsky, Eugene
  TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
  NUMBER OF SEQUENCES: 19
  CORRESPONDENCE ADDRESS:
  ADDRESSEE: Immunex Corporation, Law Department
  STREET: 51 University Street
  CITY: Seattle
  STATE: WA
  COUNTRY: USA
  ZIP: 98101
  COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: Apple Power Macintosh
  OPERATING SYSTEM: Apple Operating System 7.5.5
  SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
  CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/995,659
  FILING DATE: 22 DECEMBER 1997
  PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US/60/064,671
  FILING DATE: 14 OCTOBER 1997
  PRIOR APPLICATION DATA:
  APPLICATION NUMBER: USSN 08/813,509
  FILING DATE: 07 MARCH 1997
  PRIOR APPLICATION DATA:
  APPLICATION NUMBER: USSN 08/772,330
  FILING DATE: 23 DECEMBER 1996
  CLASSIFICATION:
  ATTORNEY/AGENT INFORMATION:
  NAME: Perkins, Patricia Anne
  REGISTRATION NUMBER: 34,693
  REFERENCE/DOCKET NUMBER: 2852-A
  TELECOMMUNICATION INFORMATION:
  TELEPHONE: (206)587-0430
  TELEFAX: (206)233-0644
  INFORMATION FOR SEQ ID NO: 13:
  SEQUENCE CHARACTERISTICS:
  LENGTH: 317 amino acids

;
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-995-659-13

Query Match
Best Local Similarity   100.0%;   Score 1319;   DB 2;   Length 317;
Matches 249; Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Qy   61  KELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSHKVSLSSWY  120
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Qy  121  HDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMYYVTKTSIK  180
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Db  189  HDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMYYVTKTSIK  248

Qy  181  IPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLDPDQDATYF  240
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Qy  241  GAFKVRDID  249
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Db  309  GAFKVRDID  317
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; Sequence 13, Application US/0921564 9A
; Patent No. 6271349
GENERAL INFORMATION:
  APPLICANT: Anderson, Dirk M.
  APPLICANT: Galibert, Laurent
  APPLICANT: Maraskovsky, Eugene
  TITLE OF INVENTION: Receptor Activator of NF-kappaB
  NUMBER OF SEQUENCES: 19
  CORRESPONDENCE ADDRESS:
  ADDRESSEE: Immunex Corporation, Law Department
  STREET: 51 University Street
  CITY: Seattle
  STATE: WA
  COUNTRY: USA
  ZIP: 98101
  COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: Apple Power Macintosh
  OPERATING SYSTEM: Apple Operating System 7.5.5
  SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
  CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/215,649A
  FILING DATE: 17-Dec-1998
  PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 08/996,139
  FILING DATE: <Unknown>
  APPLICATION NUMBER: USSN 08/813,509
  FILING DATE: 07 MARCH 1997
  APPLICATION NUMBER: USSN 08/772,330
  FILING DATE: 23 DECEMBER 1996
  CLASSIFICATION: <Unknown>
  ATTORNEY/AGENT INFORMATION:
  NAME: Perkins, Patricia Anne
  REGISTRATION NUMBER: 34,693
  REFERENCE/DOCKET NUMBER: 2851-A
  TELECOMMUNICATION INFORMATION:
  TELEPHONE: (206)587-0430
  TELEFAX: (206)233-0644
  INFORMATION FOR SEQ ID NO: 13:
  SEQUENCE CHARACTERISTICS:
  LENGTH: 317 amino acids

OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: December 21, 2005, 13:02:07 ; Search time 137,154 Seconds
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Title: US-09-211-297-39_COPY_69_317
Perfect score: 1319
Sequence: 1 YFRAQMDPNRISEDGTHCIY.........LLDPDQDATYFGAPKVRDID 249

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

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 5: /cgn2_6/ptcodata/1/pubpaa/US10B_PUBCOMB.pep:*
 6: /cgn2_6/ptcodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Match Length	DB	ID	Description
1	1319	100.0	249	4	US-10-050-902-221	Sequence 221, App
2	1319	100.0	249	4	US-10-050-898-221	Sequence 221, Appl
3	1319	100.0	249	4	US-10-289-456-82	Sequence 82, Appl
4	1319	100.0	250	4	US-10-338-785A-1	Sequence 1, Appl
5	1319	100.0	250	4	US-10-611-363-1	Sequence 1, Appli
6	1319	100.0	270	4	US-10-289-456-80	Sequence 80, Appli
7	1319	100.0	317	4	US-09-813-329-7	Sequence 7, Appl
8	1319	100.0	317	3	US-09-871-856-13	Sequence 13, Appl
9	1319	100.0	317	3	US-09-957-944-6	Sequence 6, Appl
10	1319	100.0	317	3	US-09-865-363-13	Sequence 13, Appl
11	1319	100.0	317	3	US-09-871-291-13	Sequence 13, Appl
12	1319	100.0	317	3	US-09-877-650-13	Sequence 13, Appl
13	1319	100.0	317	3	US-09-933-915A-2	Sequence 2, Appli
14	1319	100.0	317	3	US-09-151-071-10	Sequence 10, Appl
15	1319	100.0	317	4	US-10-218-547-22	Sequence 22, Appl
16	1319	100.0	317	4	US-10-405-878-13	Sequence 13, Appl
17	1319	100.0	317	4	US-10-167-182-11	Sequence 11, Appl
18	1319	100.0	317	4	US-10-310-793-28	Sequence 28, Appl
19	1319	100.0	317	4	US-10-460-623-11	Sequence 11, Appl
20	1319	100.0	317	4	US-10-289-456-79	Sequence 79, Appl
21	1319	100.0	317	4	US-10-202-062-22	Sequence 22, Appl
22	1319	100.0	317	4	US-10-664-801-2	Sequence 2, Appli
23	1319	100.0	317	4	US-10-381-160-6	Sequence 6, Appl
24	1319	100.0	317	4	US-10-799-345-12	Sequence 12, Appl
25	1319	100.0	317	5	US-10-399-116-6	Sequence 6, Appli
26	1319	100.0	317	5	US-10-802-133-13	Sequence 13, Appli
27	1319	100.0	317	5	US-10-825-898-4	Sequence 4, Appli
28	1319	100.0	317	5	US-10-854-300-11	Sequence 11, Appl
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30	1319	100.0	317	5	US-10-451-200-6	Sequence 6, Appli
31	1319	100.0	317	5	US-10-999-523-8	Sequence 8, Appli
32	1319	100.0	317	6	US-11-028-780-22	Sequence 22, Appl
33	1319	100.0	317	6	US-11-099-059-6	Sequence 6, Appl
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35	1319	100.0	317	6	US-11-142-736-7	Sequence 7, Appli
36	1301	98.6	246	4	US-10-167-182-17	Sequence 17, Appl
37	1301	98.6	246	4	US-10-440-623-17	Sequence 17, Appl
38	1301	98.6	246	5	US-10-854-300-17	Sequence 17, Appl
39	1301	98.6	246	6	US-11-135-521-17	Sequence 17, Appl
40	1293	98.0	245	3	US-09-933-915A-10	Sequence 10, Appli
41	1293	98.0	245	3	US-09-873-829-2	Sequence 2, Appli
42	1292	98.0	244	4	US-09-210-951-42	Sequence 42, Appl
43	1292	98.0	244	4	US-10-050-902-222	Sequence 222, Appl
44	1292	98.0	244	4	US-10-050-898-222	Sequence 222, App

ALIGNMENTS

RESULT 1
US-10-050-902-221
; Sequence 221, Application US/10050902
; Publication No. US20030175290A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Bachmann, Martin
; APPLICANT: Tissot, Alain
; APPLICANT: Maurer, Patrick
; APPLICANT: Lechner, Franziska
; APPLICANT: Sebbel, Peter
; APPLICANT: Piossek, Christine
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700_0190004
; CURRENT APPLICATION NUMBER: US/10/050,902
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US/10/050,902
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/326,998
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/262,379
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/288,549
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 221
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-050-902-221

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Best Local Similarity   100.0%;
Matches 249; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy   61 KELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQFFAHLTINATDIPSGSHKVSLSSWY 120
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Db   61 KELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQFFAHLTINATDIPSGSHKVSLSSWY 120

Qy 121 HDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMVYYTKTSIK 180
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Qy 181 IPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLDPDQDATYF 240
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Db    181 IPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGBEEISIEVSNPSLLDPDQDATYF 240

Qy    241 GAFKVRDID 249
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RESULT 2
US-10-050-898-221
; Sequence 221, Application No. US20030175711A1
; Publication No. US20030175711A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Bachmann, Martin
; APPLICANT: Tissot, Alain
; APPLICANT: Maurer, Patrick
; APPLICANT: Lechner, Franziska
; APPLICANT: Sebbel, Peter
; APPLICANT: Piossek, Christine
; APPLICANT: Ortmann, Rainer
; APPLICANT: Luond, Rainer
; APPLICANT: Frey, Peter
; APPLICANT: Staufenbiel, Matthias
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.0190005
; CURRENT APPLICATION NUMBER: US20030175711A1
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/262,379
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/288,549
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/326,998
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 221
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-050-898-221

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RESULT 3
US-10-289-456-82
; Sequence 82, Application US/10289456
; Publication No. US20040032112A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin
; APPLICANT: Maurer, Patrick
; APPLICANT: Spohn, Gunther
; TITLE OF INVENTION: Antigen Arrays for Treatment of Bone Disease
; FILE REFERENCE: 1700.0330001
; CURRENT APPLICATION NUMBER: US/10/289,456
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: PCT/IB02/00166
; PRIOR FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: US 10/050,902
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/396,635
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 82
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-289-456-82

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Query Match             100.0%;  Score 1319;  DB 4;  Length 249;
Best Local Similarity   100.0%;  Pred. No. 5.3e-122;
Matches 249;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

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Qy   61 KELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSHKVSLSSWY 120
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Qy  121 HDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMYVVTKTSIK 180
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Qy  241 GAFKVRDID 249
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RESULT 4
US-10-338-785A-1
; Sequence 1, Application No. US20030219864A1
; Publication No. US20030219864A1
; GENERAL INFORMATION:
; APPLICANT: Desjarlais, John R.
; APPLICANT: Hubert, Rene S.
; APPLICANT: El Yazal, Jamal
; TITLE OF INVENTION: No. US20030219864A1el Variants of RANKL Protein
; FILE REFERENCE: A-71486
; CURRENT APPLICATION NUMBER: US/10/338,785A
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US 60/345,805
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: US 60/373,453
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank Acc. No. US20030219864A1 AAB86811
; DATABASE ENTRY DATE: 1997-11-21

OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: December 21, 2005, 13:03:52 ; Search time 7.75574 Seconds
228.978 Million cell updates/sec

Title: US-09-211-297-39_COPY_69_317
Perfect score: 1319
Sequence: 1 YFRAQMDPNRISEDGTHCIY.........LLDPDQDATYFGAFKVRDID 249

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 53982 seqs, 7132107 residues

Total number of hits satisfying chosen parameters: 53982

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	AA	ID	Description
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3	235.5	17.9	266	7	US-11-082-544-10		Sequence 10, Appli
4	232.5	17.6	281	7	US-11-077-272-2		Sequence 2, Appli
5	232.5	17.6	391	7	US-11-105-172-4		Sequence 4, Appli
6	147.5	11.2	359	7	US-11-105-172-2		Sequence 2, Appli
7	134	10.2	240	6	US-10-987-663-6		Sequence 6, Appli
8	133	10.1	157	7	US-11-010-954-1		Sequence 1, Appli
9	133	10.1	157	7	US-11-053-750-1		Sequence 1, Appli
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11	133	10.1	157	7	US-11-108-001-12		Sequence 12, Appli
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15	92.5	7.0	177	6	US-10-999-866-61		Sequence 61, Appli
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17	92.5	7.0	205	6	US-10-995-561-1029		Sequence 1029, Ap
18	86.5	6.6	104	7	US-11-065-669-15		Sequence 15, Appli
19	85	6.4	220	7	US-11-054-515-3233		Sequence 3233, Ap
20	77.5	5.9	290	7	US-11-054-198-2		Sequence 2, Appli
21	77	5.8	209	7	US-10-524-198-2		Sequence 2, Appli
22	76.5	5.8	219	7	US-11-054-515-3237		Sequence 3237, Appli
23	76.5	5.8	243	7	US-11-054-515-3236		Sequence 3236, Ap
24	74.5	5.6	239	7	US-11-054-515-3232		Sequence 3232, Ap
25	74.5	5.6	943	6	US-10-475-204-34		Sequence 34, Appl
26	73.5	5.6	207	7	US-11-054-515-3234		Sequence 3234, Ap
27	73	5.5	188	7	US-11-054-515-3235		Sequence 3235, Ap
28	73	5.5	536	6	US-10-131-826A-490		Sequence 490, App
29	72	5.5	389	7	US-11-088-686-1		Sequence 1, Appli
30	72	5.5	389	7	US-11-088-686-3		Sequence 3, Appli
31	72	5.5	389	7	US-11-088-686-5		Sequence 5, Appli
32	72	5.5	389	7	US-11-088-686-7		Sequence 7, Appli
33	72	5.5	389	7	US-11-088-686-9		Sequence 9, Appli
34	72	5.5	389	7	US-11-088-686-11		Sequence 11, Appl
35	72	5.5	389	7	US-11-088-686-13		Sequence 13, Appl
36	71.5	5.4	1001	6	US-10-467-962B-81		Sequence 81, Appl
37	71.5	5.4	1151	7	US-11-128-420-10		Sequence 10, Appl
38	71.5	5.4	1467	6	US-10-507-956-1		Sequence 1, Appli
39	71	5.4	447	7	US-11-112-882-4		Sequence 4, Appli
40	70.5	5.3	369	7	US-11-055-822-32		Sequence 32, Appli
41	70.5	5.3	585	6	US-10-878-556A-42		Sequence 42, Appli
42	70	5.3	152	6	US-10-742-634-3		Sequence 3, Appli
43	70	5.3	178	6	US-10-742-634-17		Sequence 17, Appl
44	70	5.3	266	7	US-11-054-515-3229		Sequence 3229, Ap
45	70	5.3	285	6	US-10-131-826A-24		Sequence 24, Appl

ALIGNMENTS

RESULT 1
US-11-065-669-8
; Sequence 8, Application US/11065669
; Publication No. US20050244411A1
GENERAL INFORMATION:
APPLICANT: MacKay, Fabienne
APPLICANT: Kalled, Susan
TITLE OF INVENTION: BAFF, INHIBITORS THEREOF AND THEIR USE IN THE
TITLE OF INVENTION: MODULATION OF B-CELL RESPONSE
FILE REFERENCE: 08201.0024-04000
CURRENT APPLICATION NUMBER: US/11/065,669
CURRENT FILING DATE: 2005-02-24
PRIOR APPLICATION NUMBER: 10/045,574
PRIOR FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: 09/911,777
PRIOR FILING DATE: 2001-07-24
PRIOR APPLICATION NUMBER: 60/143,228
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: PCT/US00/01788
PRIOR FILING DATE: 2000-03-25
PRIOR APPLICATION NUMBER: 60/117,169
PRIOR FILING DATE: 1999-01-25
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-065-669-8

Query Match 40.8%; Score 538; DB 7; Length 109;
Best Local Similarity 75.5%; Pred. No. 1.4e-46;
Matches 108; Conservative 0; Mismatches 1; Indels 34; Gaps 2;

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Qy        93 EAQPFAHLTINATDIPSGSHKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANI 152
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Db         1 EAQPFAHLTINATDIPSGSHKVSLSSWYHDRGWGKISNM----------------YANI 43

Qy       153 CFRHETSGDLATEYLQLMYVVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGF 212
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Db        44 CFRHHETSGDLATEYLQLMVVVTKTSIKIP----------------SEFHFYSINVGGF 86

Qy       213 FKLRSGEEISIEVSNPSLLDPDQ 235
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Db        87 FKLRSGEEISIEVSNPSLLDPDQ 109
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RESULT 2

US-10-821-234-1288
; Sequence 1288, Application US/10821234
; Publication No. US20052551141A1
; GENERAL INFORMATION:
;   APPLICANT: Labat, Ivan
;   APPLICANT: Stache-Crain, Birgit
;   APPLICANT: Andarmani, Susan
;   APPLICANT: Tang, Y. Tom
;   TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
;   FILE REFERENCE: 821A
;   CURRENT APPLICATION NUMBER: US/10/821,234
;   CURRENT FILING DATE: 2004-04-07
;   PRIOR APPLICATION NUMBER: US 60/462,047
;   PRIOR FILING DATE: 2003-04-07
;   NUMBER OF SEQ ID NOS: 1704
;   SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 1288
;   LENGTH: 281
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-821-234-1288

Query Match   17.9%; Score 236.5; DB 6; Length 281;
Best Local Similarity   25.1%; Pred. No. 3.1e-16;
Matches 67; Conservative 53; Mismatches 102; Indels 45; Gaps 10;

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Qy   59 VQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF------------AHLT----IN   103
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Db  135 TLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQE   194

Qy  159 TSGDLATEYLQLMYYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSG   218
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Db  195 EIKENTKNDKQMYQYIYKYT-SYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKEN   253

Qy  219 EEISIEVSNPSLLDPDQDATYFGAFKV   245
          : | ||:||| |||||||||||||  |
Db  254 DRIFVSVTNEHLIDMDHEASFGAFLV    280
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RESULT 3
US-11-082-544-10
; Sequence 10, Application US/11082544
; Publication No. US20050249706A1
; GENERAL INFORMATION:
;   APPLICANT: Bermudes, G.
;   APPLICANT: King, I.
;   APPLICANT: Clairmont, C.
;   APPLICANT: Lin, S.
;   APPLICANT: Belcourt, M.
;   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TUMOR-TARGETED DELIVERY OF EFFECTOR MOLECULES
;   FILE REFERENCE: 8002-059
;   CURRENT APPLICATION NUMBER: US/11/082,544
;   CURRENT FILING DATE: 2005-03-17
;   PRIOR APPLICATION NUMBER: US/09/645,415
;   PRIOR FILING DATE: 2000-08-24
;   PRIOR APPLICATION NUMBER: 60/157,581
;   PRIOR FILING DATE: 1999-10-04
;   PRIOR APPLICATION NUMBER: 60/157,637
;   PRIOR FILING DATE: 1999-10-04
;   NUMBER OF SEQ ID NOS: 61
;   SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
;   LENGTH: 266
;   TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:
;   OTHER INFORMATION: Fusion construct
US-11-082-544-10

Query Match   17.9%; Score 235.5; DB 7; Length 266;
Best Local Similarity   25.3%; Pred. No. 3.6e-16;
Matches 65; Conservative 51; Mismatches 98; Indels 43; Gaps   9;

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Db   32 DKYSKSGTACF-----LKED----DSYWDPNDEESMNSPCWQVKW-------QLRQLVR    74

Qy   69 SQHIRAEKAMVDGSWLDLAKRSKLEAQPF-----------AHLT-----INATDIPSGGSHK   113
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Db   75 KMILRTSEETI-----STVQEKQONISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNE   129

Qy  114 VSL----SSWYHDR-GWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYL   168
          |     :   |     | |   |   :  ||    :  ||:|||:::::: |  :   |
Db  130 KALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDK   189

Qy  169 QLMYYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNP   228
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Qy  229 SLLLDPDQDATYFGAFKV   245
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Db  249 HLIDMDHEASFGAFLV    265
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RESULT 4
US-11-077-272-2
; Sequence 2, Application US/11077272
; Publication No. US20050244927A1
; GENERAL INFORMATION:
;   APPLICANT: LEUNG, WOON-LAM SUSAN
;   APPLICANT: SWARTZ, JAMES R.
;   TITLE OF INVENTION: PROCESS FOR PRODUCING POLYPEPTIDES
;   FILE REFERENCE: P2019R1
;   CURRENT APPLICATION NUMBER: US/11/077,272
;   CURRENT FILING DATE: 2005-03-10
;   PRIOR APPLICATION NUMBER: US 60/552,678
;   PRIOR FILING DATE: 2004-03-11
;   NUMBER OF SEQ ID NOS: 7
; SEQ ID NO 2
;   LENGTH: 281
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-077-272-2

Query Match   17.6%; Score 232.5; DB 7; Length 281;
Best Local Similarity   25.1%; Pred. No. 7.6e-16;
Matches 67; Conservative 52; Mismatches 103; Indels 45; Gaps 10;

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Db   37 YFTNELKQMQDKYSKSGTACF-----LKED----DSYWDPNDEESMNSPCWQVKW-----  82

Qy   59 VQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF------------AHLT----IN   103
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Db   83 ---QLRQLVRKMILRTSEETI-----STVQEKQONISPLVRERGPQRVAAHITGTRGRSN   134

Qy  104 ATDIPSGGSHKVSL----SSWYHDR-GWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHE   158
          :|:: :  :|  |     :   |     | |   |   :  ||    :  ||:|||:::::
Db  135 TLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHGKGFYYIYSQTYFRFQE   194

Qy  159 TSGDLATEYLQLMYYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSG   218
          : |  :   |  |  ::  ::    | :|:  |   : |   : : |  |: |:::||:|
Db  195 EIKENTKNDKQMYQYIYKYT-SYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKEN   253

Qy  219 EEISIEVSNPSLLDPDQDATYFGAFKV   245
          : | ||:||| |||||||||||||  |
Db  254 DRIFVSVTNEHLIDMDHEASFGAFLV    280
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OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: December 21, 2005, 12:44:31 ; Search time 2.89836 seconds
(without alignments)
484,925 Million cell updates/sec

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters: 572060

Searched: 572060 seqs, 82675679 residues

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Sequence: 1 VYVVKTSIKIPSSHNLM 17
Perfect score: 84
Title:

OM protein - protein search, using sw model

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	84	100.0	17	2	US-09-052-521C-35	Sequence 35, Appl
2	84	100.0	173	2	US-09-396-937-10	Sequence 10, Appl
3	84	100.0	173	2	US-09-396-937-12	Sequence 12, Appl
4	84	100.0	173	2	US-09-396-937-18	Sequence 18, Appl
5	84	100.0	188	2	US-09-396-937-8	Sequence 8, Appl
6	84	100.0	187	2	US-09-396-937-14	Sequence 14, Appl
7	84	100.0	294	2	US-08-996-139-11	Sequence 11, Appl
8	84	100.0	294	2	US-08-995-659-11	Sequence 11, Appl
9	84	100.0	294	2	US-09-215-649A-11	Sequence 11, Appl
10	84	100.0	294	2	US-09-577-780-11	Sequence 11, Appl
11	84	100.0	294	2	US-09-577-800-11	Sequence 11, Appl
12	84	100.0	294	2	US-09-466-496-11	Sequence 11, Appl
13	84	100.0	294	2	US-09-871-856-11	Sequence 11, Appl
14	84	100.0	294	2	US-09-871-291-11	Sequence 11, Appl
15	84	100.0	294	2	US-09-877-650-11	Sequence 11, Appl
16	84	100.0	294	2	US-09-865-363-11	Sequence 11, Appl
17	84	100.0	294	2	US-09-688-459-11	Sequence 11, Appl
18	84	100.0	316	1	US-08-842-842-7	Sequence 7, Appli
19	84	100.0	316	2	US-08-989-362-2	Sequence 2, Appli
20	84	100.0	316	2	US-09-052-521C-2	Sequence 2, Appli
21	84	100.0	316	2	US-09-671-658A-2	Sequence 2, Appli
22	84	100.0	316	2	US-09-396-937-4	Sequence 4, Appli
23	84	100.0	316	2	US-09-396-937-6	Sequence 6, Appli
24	84	100.0	316	2	US-09-957-944-8	Sequence 8, Appli
25	84	100.0	317	2	US-08-996-139-13	Sequence 13, Appl
26	74	88.1	317	2	US-08-995-659-13	Sequence 13, Appli
27	74	88.1	317	2	US-09-215-649A-13	Sequence 13, Appl
28	74	88.1	317	2	US-09-052-521C-4	Sequence 4, Appli
29	74	88.1	317	2	US-09-577-780-13	Sequence 13, Appl
30	74	88.1	317	2	US-09-577-800-13	Sequence 13, Appl
31	74	88.1	317	2	US-09-466-496-13	Sequence 13, Appl
32	74	88.1	317	2	US-09-871-856-13	Sequence 13, Appl
33	74	88.1	317	2	US-09-871-291-13	Sequence 13, Appl
34	74	88.1	317	2	US-09-396-937-2	Sequence 2, Appl
35	74	88.1	317	2	US-09-877-650-13	Sequence 13, Appl
36	74	88.1	317	2	US-09-865-363-13	Sequence 13, Appl
37	74	88.1	317	2	US-09-688-459-13	Sequence 13, Appl
38	74	88.1	317	2	US-09-957-944-6	Sequence 6, Appl
39	71	84.5	182	2	US-09-396-937-16	Sequence 16, Appl
40	69	82.1	173	2	US-09-396-937-20	Sequence 20, Appl
41	54	64.3	12	2	US-09-628-665-4	Sequence 4, Appl
42	54	64.2	16	2	US-09-628-665-23	Sequence 23, Appl
43	53	63.1	109	2	US-09-911-777-8	Sequence 8, Appli
44	50	59.5	10	2	US-09-628-665-6	Sequence 6, Appli
45	50	59.5	11	2	US-09-628-665-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-09-052-521C-35

; Sequence 35, Application US/09052521C
; Patent No. 6316408
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors
; FILE REFERENCE: A-451Brv
; CURRENT APPLICATION NUMBER: US/09/052,521C
; CURRENT FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 08/880,855
; PRIOR FILING DATE: 1997-06-23
; PRIOR APPLICATION NUMBER: 08/842,842
; PRIOR FILING DATE: 1997-04-16
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-052-521C-35

Query Match 100.0%; Score 84; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 VYVVKTSIKIPSSHNLM 17
        |||||||||||||||||
Db   1 VYVVKTSIKIPSSHNLM 17

RESULT 2
US-09-396-937-10

; Sequence 10, Application US/09396937
; Patent No. 6645500
; GENERAL INFORMATION:
; APPLICANT: M&E Biotech A/S
; APPLICANT: HALKIER, Torben
; APPLICANT: HAANING, Jesper
; TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 22021 PC 1
; CURRENT APPLICATION NUMBER: US/09/396,937
; CURRENT FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10

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;  LENGTH: 173
;  TYPE: PRT
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: Description of Artificial Sequence: DNA encoding
;  OTHER INFORMATION: murine OPGL, residues 158-316, fused to His tag
US-09-396-937-10

Qy    1 VYVVKTSIKIPSSHNLM 17
        |||||||||||||||||
Db   96 VYVVKTSIKIPSSHNLM 112

Query Match        100.0%;  Score 84;  DB 2;  Length 173;
Best Local Similarity  100.0%;  Pred. No. 2.1e-06;
Matches  17;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
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RESULT 3
US-09-396-937-12
Sequence 12, Application US/09396937
Patent No. 6645500
GENERAL INFORMATION:
;  APPLICANT: M&E Biotech A/S
;  APPLICANT: HALKIER, Torben
;  APPLICANT: HAANING, Jesper
;  TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
;  TITLE OF INVENTION: Activity
;  FILE REFERENCE: 22021 PC 1
;  CURRENT APPLICATION NUMBER: US/09/396,937
;  CURRENT FILING DATE: 1999-09-15
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: Patentin Ver. 2.1
;  SEQ ID NO 12
;  LENGTH: 173
;  TYPE: PRT
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: Description of Artificial Sequence: Fusion of
;  OTHER INFORMATION: murine OPGL, residues 158-316 with C to S
;  OTHER INFORMATION: mutation, and His tag
US-09-396-937-12

Qy    1 VYVVKTSIKIPSSHNLM 17
        |||||||||||||||||
Db   96 VYVVKTSIKIPSSHNLM 112

Query Match        100.0%;  Score 84;  DB 2;  Length 173;
Best Local Similarity  100.0%;  Pred. No. 2.1e-06;
Matches  17;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
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RESULT 4
US-09-396-937-18
Sequence 18, Application US/09396937
Patent No. 6645500
GENERAL INFORMATION:
;  APPLICANT: M&E Biotech A/S
;  APPLICANT: HALKIER, Torben
;  APPLICANT: HAANING, Jesper
;  TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
;  TITLE OF INVENTION: Activity
;  FILE REFERENCE: 22021 PC 1
;  CURRENT APPLICATION NUMBER: US/09/396,937
;  CURRENT FILING DATE: 1999-09-15
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: Patentin Ver. 2.1
;  SEQ ID NO 18
;  LENGTH: 173
;  TYPE: PRT
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: Description of Artificial Sequence: Fusion between
;  OTHER INFORMATION: murine OPGL, residues 158-316 with tetanus toxoid
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;  OTHER INFORMATION: P2 epitope introduced, and His tag
US-09-396-937-18

Qy    1 VYVVKTSIKIPSSHNLM 17
        |||||||||||||||||
Db   96 VYVVKTSIKIPSSHNLM 112

Query Match        100.0%;  Score 84;  DB 2;  Length 173;
Best Local Similarity  100.0%;  Pred. No. 2.1e-06;
Matches  17;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
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RESULT 5
US-09-396-937-8
Sequence 8, Application US/09396937
Patent No. 6645500
GENERAL INFORMATION:
;  APPLICANT: M&E Biotech A/S
;  APPLICANT: HALKIER, Torben
;  APPLICANT: HAANING, Jesper
;  TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
;  TITLE OF INVENTION: Activity
;  FILE REFERENCE: 22021 PC 1
;  CURRENT APPLICATION NUMBER: US/09/396,937
;  CURRENT FILING DATE: 1999-09-15
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: Patentin Ver. 2.1
;  SEQ ID NO 8
;  LENGTH: 187
;  TYPE: PRT
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: Description of Artificial Sequence: Synthetic PCR
;  OTHER INFORMATION: product with optimum codons for E. coli and P.
;  OTHER INFORMATION: pastoris expression
US-09-396-937-8

Qy    1 VYVVKTSIKIPSSHNLM 17
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Db  110 VYVVKTSIKIPSSHNLM 126

Query Match        100.0%;  Score 84;  DB 2;  Length 187;
Best Local Similarity  100.0%;  Pred. No. 2.3e-06;
Matches  17;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
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RESULT 6
US-09-396-937-14
Sequence 14, Application US/09396937
Patent No. 6645500
GENERAL INFORMATION:
;  APPLICANT: M&E Biotech A/S
;  APPLICANT: HALKIER, Torben
;  APPLICANT: HAANING, Jesper
;  TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
;  TITLE OF INVENTION: Activity
;  FILE REFERENCE: 22021 PC 1
;  CURRENT APPLICATION NUMBER: US/09/396,937
;  CURRENT FILING DATE: 1999-09-15
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: Patentin Ver. 2.1
;  SEQ ID NO 14
;  LENGTH: 188
;  TYPE: PRT
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: Description of Artificial Sequence: Fusion of
;  OTHER INFORMATION: murine OPGL, residues 158-316 modified by
;  OTHER INFORMATION: introduction of tetanus toxoid P30 epitope, and
;  OTHER INFORMATION: His tag
US-09-396-937-14

Query Match        100.0%;  Score 84;  DB 2;  Length 188;
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: December 21, 2005, 13:02:07 ; Search time 9.36393 seconds
                                                    (without alignments)
                                                    758.559 Million cell updates/sec

Title: US-09-211-297-34
Perfect score: 84
Sequence: 1 VYVVKTSIKIPSSHNLM 17

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 10%
                 Listing first 45 summaries

Database :   Published_Applications_AA_Main:*
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                4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
                5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
                6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	84	100.0	17	5	US-10-825-898-35	Sequence 35, Appl
2	84	100.0	18	5	US-10-825-898-36	Sequence 36, Appl
3	84	100.0	160	3	US-09-779-050A-14	Sequence 14, Appl
4	84	100.0	170	3	US-09-791-153A-76	Sequence 76, Appl
5	84	100.0	170	4	US-10-289-456-99	Sequence 99, Appl
6	84	100.0	173	4	US-10-664-801-10	Sequence 10, Appl
7	84	100.0	173	4	US-10-664-801-12	Sequence 12, Appl
8	84	100.0	187	4	US-10-664-801-18	Sequence 18, Appl
9	84	100.0	187	4	US-10-664-801-8	Sequence 8, Appl
10	84	100.0	188	4	US-10-664-801-14	Sequence 14, Appl
11	84	100.0	193	4	US-10-289-456-96	Sequence 96, Appl
12	84	100.0	199	4	US-10-050-902-224	Sequence 224, Appl
13	84	100.0	199	4	US-10-050-898-224	Sequence 224, App
14	84	100.0	199	4	US-10-289-456-86	Sequence 86, Appl
15	84	100.0	244	4	US-10-167-182-16	Sequence 16, Appl
16	84	100.0	244	4	US-10-460-623-16	Sequence 16, Appl
17	84	100.0	244	5	US-10-854-300-16	Sequence 16, Appl
18	84	100.0	244	6	US-11-135-521-16	Sequence 16, Appl
19	84	100.0	247	4	US-10-050-902-223	Sequence 223, App
20	84	100.0	247	4	US-10-050-898-223	Sequence 223, Appl
21	84	100.0	247	4	US-10-289-456-85	Sequence 85, Appl
22	84	100.0	249	4	US-10-338-785A-3	Sequence 3, Appli
23	84	100.0	249	4	US-10-611-363-3	Sequence 3, Appl
24	84	100.0	294	3	US-09-871-856-11	Sequence 11, Appl
25	84	100.0	294	3	US-09-865-363-11	Sequence 11, Appl
26	84	100.0	294	3	US-09-871-291-11	Sequence 11, Appl
27	84	100.0	294	3	US-09-877-650-11	Sequence 11, Appl
28	84	100.0	294	4	US-10-405-878-11	Sequence 11, Appl
29	84	100.0	294	5	US-10-802-133-11	Sequence 11, Appl
30	84	100.0	316	3	US-09-957-944-8	Sequence 8, Appli
31	84	100.0	316	3	US-09-079-569-7	Sequence 7, Appli
32	84	100.0	316	3	US-09-873-829-4	Sequence 4, Appli
33	84	100.0	316	3	US-09-933-915A-16	Sequence 16, Appl
34	84	100.0	316	4	US-10-017-910-4	Sequence 4, Appli
35	84	100.0	316	4	US-10-057-057-2	Sequence 2, Appli
36	84	100.0	316	4	US-10-105-057-2	Sequence 2, Appli
37	84	100.0	316	4	US-10-272-411-19	Sequence 19, Appl
38	84	100.0	316	4	US-10-272-328A-19	Sequence 19, Appli
39	84	100.0	316	4	US-10-326-052-2	Sequence 2, Appli
40	84	100.0	316	4	US-10-167-182-1	Sequence 1, Appli
41	84	100.0	316	4	US-10-460-623-1	Sequence 1, Appli
42	84	100.0	316	4	US-10-664-801-4	Sequence 4, Appli
43	84	100.0	316	4	US-10-664-801-6	Sequence 6, Appli
44	84	100.0	316	4	US-10-799-345-10	Sequence 10, Appli
44	84	100.0	316	5	US-10-825-898-2	Sequence 2, Appli
45	84	100.0	316	5	US-10-854-300-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-10-825-898-35

; Sequence 35, Application US/10825898
; Publication No. US20050003400A1
US-10-825-898-35

;   GENERAL INFORMATION:
;   APPLICANT: BOYLE, WILLIAM
;   TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS AND RECEPTORS
;   FILE REFERENCE: A-451K REV 09-10-03 54SEQ
;   CURRENT APPLICATION NUMBER: US/10/825,898
;   CURRENT FILING DATE: 2004-04-15
;   PRIOR APPLICATION NUMBER: US/10/825,898
;   PRIOR FILING DATE: 2004-04-15
;   PRIOR APPLICATION NUMBER: US 09/052,521
;   PRIOR FILING DATE: 1998-03-30
;   PRIOR APPLICATION NUMBER: US 08/880,855
;   PRIOR FILING DATE: 1997-06-23
;   PRIOR APPLICATION NUMBER: US 08/842,842
;   PRIOR FILING DATE: 1997-04-16
;   NUMBER OF SEQ ID NOS: 54
;   SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
;   LENGTH: 17
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Oligonucleotide
US-10-825-898-35

Query Match   100.0%; Score 84; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 VYVVKTSIKIPSSHNLM 17
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Db   1 VYVVKTSIKIPSSHNLM 17

RESULT 2
US-10-825-898-36

; Sequence 36, Application US/10825898
; Publication No. US20050003400A1
US-10-825-898-36

;   GENERAL INFORMATION:
;   APPLICANT: BOYLE, WILLIAM
;   TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS AND RECEPTORS
;   FILE REFERENCE: A-451K REV 09-10-03 54SEQ
;   CURRENT APPLICATION NUMBER: US/10/825,898
;   CURRENT FILING DATE: 2004-04-15
;   PRIOR APPLICATION NUMBER: US/10/825,898
;   PRIOR FILING DATE: 2004-04-15
;   PRIOR APPLICATION NUMBER: US 09/052,521

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;   PRIOR FILING DATE: 1998-03-30
;   PRIOR APPLICATION NUMBER: US 08/880,855
;   PRIOR FILING DATE: 1997-06-23
;   PRIOR APPLICATION NUMBER: US 08/842,842
;   PRIOR FILING DATE: 1997-04-16
;   NUMBER OF SEQ ID NOS: 54
;   SOFTWARE: Patentin version 3.1
;   SEQ ID NO 36
;     LENGTH: 18
;     TYPE: PRT
;     ORGANISM: Artificial Sequence
;     FEATURE:
;     OTHER INFORMATION: Synthetic Oligonucleotide
US-10-825-898-36

Qy          1 VYVVKTSIKIPSSHNLM 17
              |||||||||||||||||
Db          1 VYVVKTSIKIPSSHNLM 17

RESULT 3
US-09-779-050A-14
;   Sequence 14, Application US/0977905050A
;   Patent No. US20020160416A1
;   GENERAL INFORMATION:
;   APPLICANT: BOYLE, WILLIAM
;   APPLICANT: HSU, HAILING
;   TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
;   FILE REFERENCE: A-570B
;   CURRENT APPLICATION NUMBER: US/09/779,050A
;   CURRENT FILING DATE: 2001-02-12
;   PRIOR APPLICATION NUMBER: 60/181,800
;   PRIOR FILING DATE: 2000-02-11
;   NUMBER OF SEQ ID NOS: 52
;   SOFTWARE: Patentin version 3.0
;   SEQ ID NO 14
;     LENGTH: 160
;     TYPE: PRT
;     ORGANISM: Mus musculus
US-09-779-050A-14

Query Match      100.0%;   Score 84;   DB 5;   Length 18;
Best Local Similarity  100.0%;   Pred. No. 1.6e-07;
Matches  17;   Conservative  0;   Mismatches  0;   Indels  0;   Gaps  0;

Qy          1 VYVVKTSIKIPSSHNLM 17
              |||||||||||||||||
Db          1 VYVVKTSIKIPSSHNLM 17
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;     TYPE: PRT
;     ORGANISM: Mus musculus
US-09-791-153A-76

Query Match      100.0%;   Score 84;   DB 3;   Length 160;
Best Local Similarity  100.0%;   Pred. No. 1.8e-06;
Matches  17;   Conservative  0;   Mismatches  0;   Indels  0;   Gaps  0;

Qy          1 VYVVKTSIKIPSSHNLM 17
              |||||||||||||||||
Db         83 VYVVKTSIKIPSSHNLM 99

RESULT 4
US-09-791-153A-76
;   Sequence 76, Application US/0979115153A
;   Publication No. US20030103978A1
;   GENERAL INFORMATION:
;   APPLICANT: Deshpande, Rajendra
;   APPLICANT: Hitz, Anna
;   APPLICANT: Boyle, William
;   APPLICANT: Sullivan, John
;   TITLE OF INVENTION: SELECTIVE BINDING AGENTS OF OSTEOPROTEGERIN BINDING PROTEIN
;   FILE REFERENCE: A-633A
;   CURRENT APPLICATION NUMBER: US/09/791,153A
;   CURRENT FILING DATE: 2001-07-17
;   PRIOR APPLICATION NUMBER: 09/511,139
;   PRIOR FILING DATE: 2000-02-23
;   NUMBER OF SEQ ID NOS: 154
;   SOFTWARE: Patentin version 3.0
;   SEQ ID NO 76
;     LENGTH: 170
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;     TYPE: PRT
;     ORGANISM: Mus musculus
US-09-791-153A-76

RESULT 5
US-10-289-456-99
;   Sequence 99, Application US/10289456
;   Publication No. US20040033211A1
;   GENERAL INFORMATION:
;   APPLICANT: Bachmann, Martin
;   APPLICANT: Maurer, Patrick
;   APPLICANT: Spohn, Gunther
;   TITLE OF INVENTION: Antigen Arrays for Treatment of Bone Disease
;   FILE REFERENCE: 1700.0330001
;   CURRENT APPLICATION NUMBER: US/10/289,456
;   CURRENT FILING DATE: 2002-11-07
;   PRIOR APPLICATION NUMBER: PCT/IB02/00166
;   PRIOR FILING DATE: 2002-01-21
;   PRIOR APPLICATION NUMBER: US 10/050,902
;   PRIOR FILING DATE: 2002-01-18
;   PRIOR APPLICATION NUMBER: US 60/396,635
;   PRIOR FILING DATE: 2002-07-19
;   PRIOR APPLICATION NUMBER: US 60/331,045
;   PRIOR FILING DATE: 2001-11-07
;   NUMBER OF SEQ ID NOS: 170
;   SOFTWARE: Patentin version 3.2
;   SEQ ID NO 99
;     LENGTH: 170
;     TYPE: PRT
;     ORGANISM: Mus sp.
US-10-289-456-99

Query Match      100.0%;   Score 84;   DB 4;   Length 170;
Best Local Similarity  100.0%;   Pred. No. 1.9e-06;
Matches  17;   Conservative  0;   Mismatches  0;   Indels  0;   Gaps  0;

Qy          1 VYVVKTSIKIPSSHNLM 17
              |||||||||||||||||
Db         84 VYVVKTSIKIPSSHNLM 100

RESULT 6
US-10-664-801-10
;   Sequence 10, Application US/10664801
;   Publication No. US20040115199A1
;   GENERAL INFORMATION:
;   APPLICANT: M&E Biotech A/S
;   APPLICANT: HALKIER, Torben
;   APPLICANT: HAANING, Jesper
;   TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
;   FILE REFERENCE: 22021 PC 1
;   CURRENT APPLICATION NUMBER: US/10/664,801
;   CURRENT FILING DATE: 2003-09-17
;   PRIOR APPLICATION NUMBER: US/09/396,937
;   PRIOR FILING DATE: 1999-09-15
;   NUMBER OF SEQ ID NOS: 35
;   SOFTWARE: Patentin Ver. 2.1
;   SEQ ID NO 10
;     LENGTH: 173
;     TYPE: PRT
;     ORGANISM: Artificial Sequence
;     FEATURE:
;     OTHER INFORMATION: Description of Artificial Sequence: DNA encoding
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Query Match      100.0%;   Score 84;   DB 3;   Length 170;
Best Local Similarity  100.0%;   Pred. No. 1.9e-06;
Matches  17;   Conservative  0;   Mismatches  0;   Indels  0;   Gaps  0;

Qy          1 VYVVKTSIKIPSSHNLM 17
              |||||||||||||||||
Db         93 VYVVKTSIKIPSSHNLM 109
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OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: December 21, 2005, 13:03:52 ; Search time 0.529508 Seconds
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Title: US-09-211-297-34
Perfect score: 84
Sequence: 1 VYVVKTSIKIPSSHNLM 17

Scoring table: BLOSUM62
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Searched: 53982 seqs, 7132107 residues

Total number of hits satisfying chosen parameters: 53982

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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                 7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match Length	DB	ID	Description
1	53	63.1	109	7	US-11-065-669-8	Sequence 8, Appli
2	44.0	717	6	US-10-793-626-3022	Sequence 3022, Ap
3	41.7	717	6	US-11-077-550-110	Sequence 110, App
4	35	269	6	US-10-821-234-1684	Sequence 1684, Ap
5	34	113	6	US-10-793-626-3282	Sequence 3282, Ap
6	34	351	6	US-10-467-657-5088	Sequence 5088, Ap
7	33.5	374	6	US-11-060-023-10	Sequence 10, Appl
8	33	39	6	US-10-467-657-2174	Sequence 2174, Ap
9	33	96	6	US-10-467-657-8984	Sequence 8984, Ap
10	33	155	6	US-11-069-642-97	Sequence 97, Appl
11	33	198	7	US-11-069-642-25	Sequence 25, Appl
12	33	208	6	US-10-980-388-81	Sequence 81, Appl
13	33	238	7	US-11-069-642-127	Sequence 127, Appli
14	33	431	7	US-11-069-642-1	Sequence 1, Appli
15	33	437	7	US-11-069-642-92	Sequence 92, Appl
16	33	438	7	US-11-069-642-49	Sequence 49, Appl
17	33	438	7	US-11-069-642-51	Sequence 51, Appl
18	33	438	7	US-11-069-642-53	Sequence 53, Appl
19	33	438	7	US-11-069-642-55	Sequence 55, Appl
20	33	438	7	US-11-069-642-57	Sequence 57, Appl
21	33	438	7	US-11-069-642-59	Sequence 59, Appl
22	33	438	7	US-11-069-642-61	Sequence 61, Appl
23	33	438	7	US-11-069-642-63	Sequence 63, Appl
24	33	490	7	US-11-131-826A-310	Sequence 310, Appl
25	33	619	6	US-10-763-712A-35	Sequence 35, Appl
26	33	734	7	US-11-093-274-40	Sequence 40, Appl
27	39.3	949	7	US-11-077-550-68	Sequence 68, Appl
28	39.3	1420	7	US-11-077-550-110	Sequence 110, App
29	38.1	64	6	US-10-467-657-7122	Sequence 7122, Ap
30	38.1	101	7	US-11-053-076-51	Sequence 51, Appl
31	38.1	111	7	US-11-053-076-163	Sequence 163, App
32	38.1	215	6	US-10-793-626-596	Sequence 596, App
32	38.1	215	6	US-10-793-626-2258	Sequence 2258, Ap
33	38.1	257	6	US-10-467-962B-73	Sequence 73, Appl
34	38.1	317	6	US-10-689-742-166	Sequence 166, App
35	38.1	356	7	US-11-055-822-972	Sequence 972, App
36	38.1	356	7	US-11-055-822-1052	Sequence 1052, Ap
37	38.1	437	7	US-11-082-389-180	Sequence 180, App
38	38.1	477	7	US-11-055-822-970	Sequence 970, App
39	38.1	477	7	US-11-055-822-1050	Sequence 1050, App
40	38.1	478	6	US-10-793-626-768	Sequence 768, App
41	38.1	567	6	US-10-131-826A-476	Sequence 476, App
42	38.1	1234	7	US-11-067-657-4224	Sequence 4224, Ap
43	38.1	2725	7	US-11-113-424-52	Sequence 52, Appl
44	38.1	2725	6	US-11-467-657-4224	Sequence 4224, App
45	36.9	102	7	US-11-053-076-162	Sequence 162, App

ALIGNMENTS

RESULT 1
US-11-065-669-8
; Sequence 8, Application US/11065669
; Publication No. US20050244411A1
; GENERAL INFORMATION:
; APPLICANT: MacKay, Fabienne
; APPLICANT: Kalled, Susan
; TITLE OF INVENTION: BAFF, INHIBITORS THEREOF AND THEIR USE IN THE
; TITLE OF INVENTION: MODULATION OF B-CELL RESPONSE
; FILE REFERENCE: 08201.0024-04000
; CURRENT APPLICATION NUMBER: US/11/065,669
; CURRENT FILING DATE: 2005-02-24
; PRIOR APPLICATION NUMBER: 10/045,574
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US00/01788
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/117,169
; PRIOR FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 8
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-065-669-8

Query Match   63.1%; Score 53; DB 7; Length 109;
Best Local Similarity   91.7%; Pred. No. 0.0067;
Matches   11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy   1 VYVVKTSIKIPS 12
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Db   63 VYVVKTSIKIPS 74

RESULT 2
US-10-793-626-3022
; Sequence 3022, Application US/10793626
; Publication No. US20050254578A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626

CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3022
; LENGTH: 717
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-3022

Qy   2 YVVKTSIKIPSSH 14
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Db   198 YIVKQGVKILNNH 210

RESULT 3
US-10-821-234-1684
; Sequence 1684, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 1684
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1684

Query Match   44.0%; Score 37; DB 6; Length 269;
Best Local Similarity   46.2%;
Matches   6; Conservative   4; Mismatches   3; Indels   0; Gaps   0;

Qy   2 YVVKTSIKIPSSH 14
          ||||| ||| ||:
Db   186 TDIKIATGHNII 197

RESULT 4
US-10-793-626-3282
; Sequence 3282, Application US/10793626
; Publication No. US20050254780A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3282
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-3282

Query Match   40.5%; Score 34; DB 6; Length 113;
Best Local Similarity   42.9%;
Matches   6; Conservative   4; Mismatches   4; Indels   0; Gaps   0;

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          :|:| | :|:||
Db   56 VSVASTLMKLPNTH 69

RESULT 5
US-10-467-657-5088
; Sequence 5088, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5088
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5088

Query Match   40.5%; Score 34; DB 6; Length 351;
Best Local Similarity   40.0%;
Matches   6; Conservative   4; Mismatches   5; Indels   0; Gaps   0;

Qy   2 YVVKTSIKIPSSHNL 16
          :||| | || |||
Db   275 HIINPNNKRPISHNL 289

RESULT 6
US-11-060-023-10
; Sequence 10, Application US/11060023
; Publication No. US20050255531A1
; GENERAL INFORMATION:
; APPLICANT: Aventis Pharma Deutschland GmbH
; TITLE OF INVENTION: Process for identifying modulators of G protein coupled receptors
; FILE REFERENCE: AVE D-2000/A033 englisch
; CURRENT APPLICATION NUMBER: US/11/060,023
; CURRENT FILING DATE: 2005-02-17
; PRIOR APPLICATION NUMBER: US/09/899,295
; PRIOR FILING DATE: 2003-07-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 10
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-060-023-10

Query Match   39.9%; Score 33.5; DB 7; Length 374;
Best Local Similarity   47.1%;
Matches   8; Conservative   4; Mismatches   2; Indels   3; Gaps   1;

Qy   1 VYVVKTSI--KIPSSH 14

OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: December 21, 2005, 12:34:10 ; Search time 11.5656 Seconds
                    (without alignments)
                    645.834 Million cell updates/sec

Title: US-09-211-297-34
Perfect score: 84
Sequence: 1 VYVVKTSIKIPSSHNLM 17
Scoring table: BLOSUM62
                    Gapop 10.0 , Gapext 0.5
Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   A_Geneseq_21:*

                    1: geneseqp1980s:*
                    2: geneseqp1990s:*
                    3: geneseqp2000s:*
                    4: geneseqp2001s:*
                    5: geneseqp2002s:*
                    6: geneseqp2003as:*
                    7: geneseqp2003bs:*
                    8: geneseqp2004s:*
                    9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	84	100.0	17	2	AAW83198	Aaw83198 Murine os
2	84	100.0	18	2	AAW83199	Aaw83199 Murine os
3	84	100.0	139	3	AAY91023	Aay91023 Mouse OBM
4	84	100.0	155	6	ABR39854	Abr39854 RANK liga
5	84	100.0	155	7	ADC03334	Adc03334 Murine re
6	84	100.0	155	7	ADI53055	Adi53055 Human RAN
7	84	100.0	160	3	AAB08272	Aab08272 Amino aci
8	84	100.0	170	4	AAU08386	Aau08386 Mouse PLA
9	84	100.0	170	3	ADJ82132	Adj82132 Protein f
10	84	100.0	173	3	AAY84422	Aay84422 A murine
11	84	100.0	173	3	AAY84425	Aay84425 DNA encod
12	84	100.0	173	3	AAY84421	Aay84421 Amino aci
13	84	100.0	187	3	AAY84420	Aay84420 Amino aci
14	84	100.0	188	7	AAY84423	Aay84423 An osteop
15	84	100.0	193	7	ADJ82129	Adj82129 Protein f
16	84	100.0	199	5	ABG94285	Abg94285 Mouse RAN
17	84	100.0	199	5	ABG80597	Abg80597 Mouse rec
18	84	100.0	199	7	ADJ82219	Adj82219 Protein f
19	84	100.0	216	7	ADB16999	Adb16999 Murine RA
20	84	100.0	244	2	AAW83019	Aaw83019 A murine
21	84	100.0	247	5	ABG94284	Abg94284 Mouse RAN
22	84	100.0	247	5	ABG80596	Abg80596 Mouse rec
23	84	100.0	247	7	ADJ82118	Adj82118 Protein f
24	84	100.0	249	6	ADA50081	Ada50081 Mouse wil
25	84	100.0	294	2	AAW69956	Aaw69956 NF-kB rec
26	84	100.0	294	2	AAW68292	Aaw68292 NF-kB rec
27	84	100.0	294	2	AAE08737	Aae08737 Murine re
28	84	100.0	294	2	AAE04425	Aae04425 Murine re
29	84	100.0	294	4	AAE01992	Aae01992 Murine RA
30	84	100.0	294	5	AAE26102	Aae26102 Mouse RAN
31	84	100.0	294	7	ADB16986	Adb16986 Murine re
32	84	100.0	294	7	ADC73000	Adc73000 Murine RA
33	84	100.0	294	7	ADC78266	Adc78266 Murine RA
34	84	100.0	294	9	ADG46721	Adg46721 Murine RA
35	84	100.0	316	2	ADW09027	Adw09027 Murine re
36	84	100.0	316	2	AAW83017	Aaw83017 Osteoclas
37	84	100.0	316	2	AAW83194	Aaw83194 Human ost
38	84	100.0	316	2	AAW59654	Aaw59654 Amino aci
39	84	100.0	316	2	AAY17874	Aay17874 Murine TR
40	84	100.0	316	3	AAY91024	Aay91024 Mouse OBM
41	84	100.0	316	3	AAY84418	Aay84418 Amino aci
42	84	100.0	316	3	AAY84419	Aay84419 Amino aci
43	84	100.0	316	5	AAU78289	Aau78289 Mouse TRA
44	84	100.0	316	5	ADR29338	Adr29338 Mouse RAN
45	84	100.0	316	6	ABR42071	Abr42071 Human RAN

ALIGNMENTS

RESULT 1
AAW83198
ID   AAW83198 standard; peptide; 17 AA.
XX
AC   AAW83198;
XX
DT   11-FEB-1999 (first entry)
XX
DE   Murine osteoprotegerin binding protein EF loop peptide.
XX
KW   Osteoprotegerin binding protein; OPG binding protein; arthritis;
KW   osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR;
KW   hypercalcaemia; osteoclast differentiation and activation receptor;
KW   Paget's disease.
XX
OS   Mus sp.
XX
PN   WO9846751-A1.
XX
PD   22-OCT-1998.
XX
PF   15-APR-1998;   98WO-US007584.
XX
PR   16-APR-1997;   97US-00842842.
PR   23-JUN-1997;   97US-00880855.
PR   30-MAR-1998;   98US-00052521.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Boyle WJ;
XX
DR   WPI; 1998-594578/50.
XX
PT   Nucleic acid encoding osteoprotegerin binding protein - useful for, e.g.
PT   treating bone diseases by modulating osteoclast differentiation and for
PT   diagnosis.
XX
PS   Example 11; Page 55; 47pp; English.
XX
CC   The present sequence represents peptide from murine osteoprotegerin (OPG)
CC   binding protein. Host cells transfected with vectors containing nucleic
CC   acid molecules encoding OPG binding protein are used to produce
CC   recombinant OPG binding protein. OPG binding protein is used in binding
CC   assays to determine osteoprotegerin (OG) in biological samples; to screen
CC   for specific binding agents (particularly agonists and antagonists,
CC   including intracellular proteins); to raise Ab (useful in immunoassays
CC   for detection of OPG binding protein) and to identify compounds that

CC   modulate binding of OPG binding protein to osteoclast differentiation and
CC   activation receptor (ODAR). The nucleic acid molecule encoding OPG
CC   binding protein can be used to detect OPG binding protein-encoding
CC   sequences, e.g. screening for related sequences, also to produce
CC   transgenic animal models, while complementary sequences are used for
CC   antisense regulation of OPG binding protein expression. Modulators of OPG
CC   binding protein, particularly soluble forms of OPG binding protein or Ab,
CC   are used to treat or prevent bone diseases, e.g. osteoporosis, bone loss
CC   caused by arthritis or metastases, hypercalcaemia, Paget's disease,
CC   periodontal disease, osteoporosis, loosening of prostheses, optionally in
CC   combination with agents that promote bone growth
XX
SQ   Sequence 17 AA;

Query Match   100.0%; Pred. No. 1.4e-07; Score 84; DB 2; Length 17;
Best Local Similarity   100.0%;
Matches   17; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 VYVVKTSIKIPSSHNLM 17
              |||||||||||||||||
Db   1 VYVVKTSIKIPSSHNLM 17

RESULT 2
AAW83199
ID   AAW83199 standard; peptide; 18 AA.
XX
AC   AAW83199;
XX
DT   11-FEB-1999 (first entry)
XX
DE   Murine osteoprotegerin binding protein EF loop-Cys peptide.
XX
KW   Osteoprotegerin binding protein; OPG binding protein; arthritis;
KW   osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR;
KW   hypercalcaemia; osteoclast differentiation and activation receptor;
KW   Paget's disease.
XX
OS   Mus sp.
XX
XX
PN   WO9846751-A1.
XX
PD   22-OCT-1998.
XX
PF   15-APR-1998; 98WO-US007584.
XX
PR   16-APR-1997; 97US-00842842.
PR   23-JUN-1997; 97US-00880855.
PR   30-MAR-1998; 98US-00052521.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Boyle WJ;
XX
DR   WPI; 1998-594578/50.
XX
PT   Nucleic acid encoding osteoprotegerin binding protein - useful for, e.g.
PT   treating bone diseases by modulating osteoclast differentiation and for
PT   diagnosis.
XX
PS   Example 11; Page 55; 47pp; English.
XX
CC   The present sequence represents peptide from murine osteoprotegerin (OPG)
CC   binding protein. Host cell transfected with vectors containing nucleic
CC   acid molecules encoding OPG binding protein are used to produce
CC   recombinant OPG binding protein. OPG binding protein is used in binding
CC   assays to determine osteoprotegerin (OG) in biological samples; to screen
CC   for specific binding agents (particularly agonists and antagonists,
CC   including intracellular proteins); to raise Ab (useful in immunoassays
CC   for detection of OPG binding protein) and to identify compounds that
CC   modulate binding of OPG binding protein to osteoclast differentiation and
CC   activation receptor (ODAR). The nucleic acid molecule encoding OPG
CC   'binding protein can be used to detect OPG binding protein-encoding
CC   sequences, e.g. screening for related sequences, also to produce
CC   transgenic animal models while complementary sequences are used for
CC   antisense regulation of OPG binding protein expression. Modulators of OPG
CC   binding protein, particularly soluble forms of OPG binding protein or Ab,
CC   are used to treat or prevent bone diseases, e.g. osteoporosis, bone loss
CC   caused by arthritis or metastases, hypercalcaemia, Paget's disease,
CC   periodontal disease, osteoporosis, loosening of prostheses, optionally in
CC   combination with agents that promote bone growth
XX
SQ   Sequence 18 AA;

Query Match   100.0%; Pred. No. 1.4e-07; Score 84; DB 2; Length 18;
Best Local Similarity   100.0%;
Matches   17; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 VYVVKTSIKIPSSHNLM 17
              |||||||||||||||||
Db   1 VYVVKTSIKIPSSHNLM 17

RESULT 3
AAY91023
ID   AAY91023 standard; protein; 139 AA.
XX
AC   AAY91023;
XX
DT   05-SEP-2000 (first entry)
XX
DE   Mouse OBM protein sequence SEQ ID NO:8.
XX
KW   Mouse; osteoclastogenesis inhibitory factor binding molecule; OCIF; OBM;
KW   osteoclast; bone absorption promoting factor; vitamin D3; PTH;
KW   parathyroid hormone.
XX
OS   Mus sp.
XX
PN   JP2000102390-A.
XX
PD   11-APR-2000.
XX
PF   30-SEP-1998; 98JP-00292971.
XX
PR   30-SEP-1998; 98JP-00292971.
XX
PA   (SNOW) SNOW BRAND MILK PROD CO LTD.
PA   (YSNE-) YS NEW TECHNOLOGY KENKYUSHO.
XX
DR   WPI; 2000-332087/29.
DR   N-PSDB; AAA39155.
XX
PT   A DNA and preparation of a protein by using it.
XX
PS   Example 2; Page 14; 18pp; Japanese.
XX
CC   The present invention describes a genomic DNA encoding a protein having
CC   an activity of supporting or promoting differentiation and maturation of
CC   osteoclasts. The genomic DNA encoding a protein has the following
CC   properties: (a) combines specifically with osteoclastogenesis inhibitory
CC   factor (OCIF) and has a high affinity; (b) shows a molecular weight (mw)
CC   of 30,000 to 40,000 by SDS-PAGE (sodium dodecyl sulfate-polyacrylamide
CC   gel electrophoresis) under a nonreductive condition and the apparent mw
CC   when crosslinked with monomer type OCIF is 90,000 to 110,000; and (c) has
CC   an activity of supporting or promoting differentiation and maturation of
CC   osteoclast in the co-culture of mouse osteoblast-like stroma cell and
CC   mouse spleen cell in the presence of a bone absorption promoting factor
CC   such as active type vitamin D3 and parathyroid hormone. The present
CC   can be used as a drug and a research reagent. The present invention
CC   represents a mouse OCIF binding molecule (OBM) from the present invention
XX
SQ   Sequence 139 AA;

Query Match   100.0%; Pred. No. 1.5e-06; Score 84; DB 3; Length 139;
Best Local Similarity   100.0%;

OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: December 21, 2005, 12:47:51 ; Search time 1.92295 Seconds
                 (without alignments)
                 850.612 Million cell updates/sec

Scoring table: US-09-211-297-34

Title: 84
Perfect Score: 1 VYVVKTSIKIPSSHNLM 17
Sequence:

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR_80:*
                 1: pir1:*
                 2: pir2:*
                 3: pir3:*
                 4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	45	53.6	206	2	G86279	F14L17.27 protein
2	44.5	53.0	311	2	B70441	ribose-phosphate d
3	43	51.2	232	1	I83349	CS6 subunits chape
4	43	51.2	377	2	S67448	hypothetical prote
5	41	48.8	612	2	AI3493	oligopeptide-bindi
6	40	47.6	115	2	F81358	probable periplasm
7	40	47.6	311	2	C23701	olfactory receptor
8	40	47.6	1235	2	T17457	SARA protein - Afr
9	39.5	47.0	917	2	T05430	hypothetical prote
10	39	46.4	176	2	C86824	DNA-directed RNA p
11	39	46.4	262	2	T49066	hypothetical prote
12	39	46.4	288	2	B98278	hypothetical prote
13	39	46.4	288	2	AI3005	conserved hypothet
14	39	46.4	334	2	A70101	hypothetical prote
15	39	46.4	360	2	T15639	hypothetical prote
16	39	46.4	603	2	T40528	palmitoyl-protein
17	39	46.4	659	2	F72568	probable acylamino
18	39	46.4	799	2	B71478	probable cell divi
19	39	46.4	1109	2	B90127	hypothetical prote
20	39	46.4	1227	2	T48028	hypothetical prote
21	39	46.4	1802	2	S69703	HKR1 protein precu
22	38.5	45.8	400	2	A46297	beta-1,6-N-acetylg
23	38.5	45.8	699	2	T16109	hypothetical prote
24	38	45.2	135	2	PN0530	G protein-coupled
25	38	45.2	294	2	B69445	conserved hypothet
26	38	45.2	332	2	H84129	sugar ABC transpor
27	38	45.2	510	1	S15620	L1 protein - human
28	38	45.2	672	2	E90294	hypothetical prote
29	38	45.2	899	2	G71453	hypothetical prote
30	38	45.2	1038	2	S52522	hypothetical prote
31	38	45.2	1517	2	T38912	hypothetical integ
32	37.5	44.6	119	2	AH3459	hypothetical prote
33	37	44.0	72	2	AH2528	hypothetical prote
34	37	44.0	76	2	AH2120	uncharacterized co
35	37	44.0	174	2	F97114	hypothetical prote
36	37	44.0	291	2	S28299	hypothetical prote
37	37	44.0	307	2	T34143	hypothetical prote
38	37	44.0	327	2	G83921	hypothetical prote
39	37	44.0	334	2	E75153	probable flagellar
40	37	44.0	370	2	S52699	hypothetical prote
41	37	44.0	377	2	AB0087	glyceraldehyde 3-p
42	37	44.0	433	2	AD1164	H-transporting AT
43	37	44.0	433	2	AD1523	H-transporting AT
44	37	44.0	452	2	JC6561	UDP-N-acetylmuramo
45	37	44.0	506	1	ACRYG1	nicotinic acetylch

ALIGNMENTS

RESULT 1
G86279
F14L17.27 protein - Arabidopsis thaliana
G86279
F14L17.27 protein - Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: G86279
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.;
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: G86279
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-206 <STO>
A;Cross-references: UNIPROT:Q9M9R4; UNIPARC:UPI000000A0A22; GB:AE005172; NID:g7262692; PI
C;Genetics:
A;Map position: 1

Query Match   53.6%;   Score 45;   DB 2;   Length 206;
Best Local Similarity   62.5%;   Pred. No. 2.5;
Matches   10;   Conservative   0;   Mismatches   6;   Indels   0;   Gaps   0;

Qy   1 VYVVKTSIKIPSSHNL 16
              ||||:|| | | |||
Db   142 VYFVATSFKNPSYHRL 157

RESULT 2
B70441
ribose-phosphate diphosphokinase (EC 2.7.6.1) - Aquifex aeolicus
N;Alternate names: Phosphoribosylpyrophosphate synthetase
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: B70441
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
V.
Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: B70441
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-311 <AQF>
A;Cross-references: UNIPROT:O67556; UNIPARC:UPI00005668B; GB:AE000748; NID:g2983960; P1
A;Experimental source: strain VF5

C;Genetics:
A;Gene: prs
C;Function:
A;Pathway: nucleotide biosynthesis
C;Superfamily: ribose-phosphate pyrophosphokinase catalytic chain
A;Pathway: diphosphotransferase; magnesium; nucleotide biosynthesis
C;Keywords: diphosphotransferase; magnesium; nucleotide binding
F;215-227//Region: phosphoribosylpyrophosphate binding

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Query Match          53.0%;  Score 44.5; DB 2;  Length 311;
Best Local Similarity 58.8%;  Pred. No. 4.7;
Matches   10;  Conservative  3;  Mismatches  3;  Indels  1;  Gaps  1;

Qy  1 VVVKTSIKIPSSHNLM 17
        ||:|:|| :|||||
Db 53 VTVI-TSLSNPVNHNLM 68
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RESULT 3
I83349
CS6 subunits chaperone - Escherichia coli
C;Species: Escherichia coli
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: I83349
R;Willshaw, G.A.; Smith, H.R.; McConnell, M.M.; Rowe, B.
FEMS Microbiol. Lett. 49, 473-478, 1988
A;Title: Cloning of genes encoding coli-surface (CS) antigens in enterotoxigenic Escheri
A;Reference number: 160266
A;Accession: I83349
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-232 <RES>
A;Cross-references: UNIPROT:P53518; UNIPARC:UPI000001284F5; EMBL:U04844; NID:g442375; PID
C;Superfamily: chaperone protein papD
C;Keywords: molecular chaperone

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Query Match          51.2%;  Score 43; DB 1;  Length 232;
Best Local Similarity 41.2%;  Pred. No. 6.3;
Matches   7;  Conservative  5;  Mismatches  5;  Indels  0;  Gaps  0;

Qy  1 VVVKTSIKIPSSHNLM 17
        |:| | ||| ||||
Db 83 IKIKTNIKLPDSQESM 99
```

RESULT 4
S67448
hypothetical protein YOR322c homolog SPAC1F12.05 - fission yeast (Schizosaccharomyces po
C;Species: Schizosaccharomyces pombe
C;Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
A;Reference number: 221766
A;Accession: S67448; T38063
R;McLean, J.; Harris, D.
submitted to the EMBL Data Library, March 1996
A;Reference number: S67448
A;Accession: S67448
A;Molecule type: DNA
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-377 <MC2>
A;Cross-references: UNIPROT:Q10347; UNIPARC:UPI000013A8E4; EMBL:Z69944; NID:g1217974; PI
R;McLean, J.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, March 1996
A;Reference number: 221766
A;Molecule type: DNA
A;Residues: 1-377 <MCL>
A;Cross-references: UNIPROT:Q10347; UNIPARC:UPI000013A8E4; EMBL:Z69944; PIDN:CAA93809.1; GSPDB:GN00066;
A;Experimental source: strain 972h-; cosmid c1F12
C;Genetics:
A;Gene: SPAC1F12.05

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Query Match          51.2%;  Score 43; DB 2;  Length 377;
Best Local Similarity 63.6%;  Pred. No. 11;
Matches   7;  Conservative  3;  Mismatches  1;  Indels  0;  Gaps  0;

Qy  1 VVVKTSIKIPS 12
        |:|| :||||
Db 131 YILKTRVKIPS 141
```

RESULT 5
AI3493
oligopeptide-binding protein appA precursor [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AI3493
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitensi
A;Cross-references: UNIPROT:Q8YEE3; UNIPARC:UPI0000058272; GB:AE008917; PIDN:AAL53116.1;
A;Experimental source: strain 16M
C;Genetics:
A;Accession: AI3493
A;Gene: BMEI1935
A;Reference number: AD3252; PMID:11756688
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-612 <KUR>
A;Map position: I
C;Superfamily: periplasmic oligopeptide-binding protein

```
Query Match          48.8%;  Score 41; DB 2;  Length 612;
Best Local Similarity 80.0%;  Pred. No. 41;
Matches   8;  Conservative  0;  Mismatches  2;  Indels  0;  Gaps  0;

Qy  7 SIKIPSSHNL 16
        |||||:|||
Db 524 SAKIPGSHNL 533
```

RESULT 6
F81358
probable periplasmic protein Cj0854c [imported] - Campylobacter jejuni (strain NCTC 11168
C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
A;Accession: F81358
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel
Nature 403, 665-668, 2000
A;Reference number: A81250; MUID:20150912; PMID:10688204
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hype
A;Accession: F81358
A;Molecule type: DNA
A;Status: preliminary
A;Residues: 1-115 <PAR>
A;Cross-references: UNIPROT:Q9PP69; UNIPARC:UPI00000C1D64; GB:AL139076; GB:AL111168; NID
A;Experimental source: serotype O2; strain NCTC 11168
A;Gene: Cj0854c
C;Superfamily: Helicobacter pylori hypothetical protein jhp0221

```
Query Match          47.6%;  Score 40; DB 2;  Length 115;
Best Local Similarity 53.8%;  Pred. No. 10;
Matches   7;  Conservative  3;  Mismatches  3;  Indels  0;  Gaps  0;

Qy  4 VKTSIKIPSSHNL 16
        ||:|||||
Db 59 IKTAYKVPSIQNL 71
```

RESULT 7
C23701
olfactory receptor F6 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004
C;Accession: C23701

```
OM protein - protein search, using sw model

                        Copyright (c) 1993 - 2005 Compugen Ltd.        GenCore version 5.1.6

Run on:            December 21, 2005, 12:35:06 ; Search time 11.7049 Seconds
                   (without alignments)
                   1024.696 Million cell updates/sec

Title:             US-09-211-297-34
Perfect score:     84
Sequence:          1 VYVVKTSIKIPSSHNLM 17

Scoring table:     BLOSUM62
                   Gapop 10.0 , Gapext 0.5

Searched:          2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters:           2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :         UniProt_05.80:*
                   1: uniprot_sprot:*
                   2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

SUMMARIES

```
Result                  %
 No.  Score  Match  Query     DB  ID              Description
                    Length
------------------------------------------------------------------------
   1    84   100.0    316      1  TNF11_MOUSE     O35235 m tumor nec
   2    84   100.0    318      1  TNF11_RAT       Q6ee2 r tumor nec
   3    74    88.1    244      1  Q5A98_HUMAN     Q5a98 homo sapien
   4.   74    88.1    317      1  TNF11_HUMAN     O14788 h tumor nec
   5    74    88.1    317      2  Q5T9Y4_HUMAN    Q5t9y4 homo sapien
   6    47    56.0    378      2  Q5L899_BACFN    Q5l899 bacteroides
   7    47    56.0    378      2  Q64NJ9_BACFR    Q64nj9 bacteroides
   8    45    53.6    206      2  Q9M9R4_ARATH    Q9m9r4 arabidopsis
   9    45    53.6    312      2  Q8VG2_MOUSE     Q8vgj2 mus musculu
  10    45    53.6    315      2  Q7TRH2_MOUSE    Q7trh2 mus musculu
  11    45    53.6    315      2  Q8VFU3_MOUSE    Q8vfu3 mus musculu
  12    45    53.6    315      2  Q8VFU4_MOUSE    Q8vfu4 mus musculu
  13    45    53.6    320      2  Q8VF26_MOUSE    Q8vf26 mus musculu
  14    45    53.0    311      1  KPRS_AQUAE      O67556 aquifex aeo
 44.5   45    53.0    311      2  Q8VGC2_MOUSE    Q8vgc2 mus musculu
  15    44    52.4    406      2  Q9LKA2_ARATH    Q9lka2 arabidopsis
  16    44    52.4    311      2  Q8LPR5_ARATH    Q8lpr5 arabidopsis
  17    44    52.4    420      2  ACHE_XENLA      P49580 xenopus lae
  18    44    52.4    504      1  Q9W7F9_CHICK    Q9w7f9 gallus gall
  19    44    52.4    727      2  Q6VZE6_CNPV     Q6vze6 canarypox v
  20    43    51.2    192      2  CSSC1_ECOLI     P53518 escherichia
  21    43    51.2    232      1  Q923H4_MOUSE    Q923h4 mus musculu
  22    43    51.2    350      2  YDAS_SCHPO      Q10347 schizosacch
  23    43    51.2    377      1  ATG8_PICPA      Q9k571 pichia past
  24    43    51.0    176      2  Q9K571_LACLC    Q9k571 lactococcus
  25    42    50.0    205      2  Q8NA88_HUMAN    Q8na88 homo sapien
  26    42    50.0    205      2  Q6QA70_HUMAN    Q6qa70 homo sapien
  27    42    50.0    225      2  Q8NGU1_HUMAN    Q8ngu1 homo sapien
  28    42    50.0    225      2  Q8NGU1_HUMAN    Q8ngu1 homo sapien
  29    42    50.0    288      2  Q6W061_MOUSE    Q6w061 mus musculu
  30    42    50.0    310      2  Q8VFD8_MOUSE    Q8vfd8 mus musculu
  31    42    50.0    312      2  Q8VFH8_MOUSE    Q8vfh8 mus musculu
  32    42    50.0    314      1  OR9A4_HUMAN     Q8ngu2 homo sapien
  33    42    50.0    314      2  Q6IFI4_HUMAN    Q6ifi4 homo sapien
  34    42    50.0    336      2  Q6FQE8_CANGA    candida gla
  35    42    50.0    485      2  Q59WH5_CANAL    Q59wh5 candida alb
  36    42    50.0    505      2  Q6S3H5_CHON     Q6s3h5 hypnos mono
  37    42    50.0    530      2  Q8IJ67_PLAF7    Q8ij67 plasmodium
  38    42    50.0    778      1  DACT1_MOUSE     Q8r4a3 mus musculu
  39    42    50.0    836      1  DACT1_HUMAN     Q9nyf0 homo sapien
  40    42    50.0    877      2  Q5CTV9_CRYPV    Q5ctv9 cryptospori
  41    42    50.0    892      2  Q5CMP0_CRYHO    Q5cmp0 cryptospori
  42    42    50.0    992      1  ANR18_HUMAN     Q8ivf6 homo sapien
  42    42    50.0    992      1  Q5SY86_HUMAN    Q5sy86 homo sapien
  43    42    50.0    997      2  Q5SY86_HUMAN    Q5sy86 homo sapien
  44    42    50.0   1072      2  Q4WRN9_ASPFU    Q4wrn9 aspergillus
  45    42    50.0   1776      2  Q7R2L9_GIALA    Q7r219 giardia lam
```

ALIGNMENTS

RESULT 1
```
TNF11_MOUSE
ID   TNF11_MOUSE              STANDARD;      PRT;    316 AA.
AC   O35235; O35306; Q9JJK8; Q9JJK9; Q9R1Y0;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Tumor necrosis factor ligand superfamily member 11 (Receptor activator
DE   of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-
DE   induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast
DE   differentiation factor) (ODF) [Contains: Tumor necrosis factor ligand
DE   superfamily member 11, membrane form; Tumor necrosis factor ligand
DE   superfamily member 11, soluble form].
GN   Name=Tnfsf11; Synonyms=Opgl, Rankl, Trance;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE (ISOFORM 1).
RC   TISSUE=Hybridoma;
RX   MEDLINE=97460112; PubMed=9312132; DOI=10.1074/jbc.272.40.25190;
RA   Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M.,
RA   Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
RA   Choi Y.;
RT   "TRANCE is a novel ligand of the tumor necrosis factor receptor family
RT   that activates c-Jun N-terminal kinase in T cells.";
RL   J. Biol. Chem. 272:25190-25194(1997).
RN   [2]
RP   NUCLEOTIDE SEQUENCE (ISOFORM 1).
RC   TISSUE=Thymic lymphoma;
RX   MEDLINE=98032977; PubMed=9367155; DOI=10.1038/36593;
RA   Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
RA   Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
RA   Galibert L.;
RT   "A homologue of the TNF receptor and its ligand enhance T-cell growth
RT   and dendritic-cell function.";
RL   Nature 390:175-179(1997).
RN   [3]
RP   NUCLEOTIDE SEQUENCE (ISOFORM 1).
RC   TISSUE=Bone marrow;
RX   MEDLINE=98227661; PubMed=9568710; DOI=10.1016/S0092-8674(00)81569-X;
RA   Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,
RA   Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,
RA   Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,
RA   Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,
RA   Boyle W.J.;
RT   "Osteoprotegerin ligand is a cytokine that regulates osteoclast
RT   differentiation and activation.";
RL   Cell 93:165-176(1998).
RN   [4]
RP   NUCLEOTIDE SEQUENCE (ISOFORM 1).
RC   TISSUE=Bone marrow stroma;
```

```
RX   MEDLINE=98188248; PubMed=9520411; DOI=10.1073/pnas.95.7.3597;
RA   Yasuda H., Shima N., Nakagawa N., Yamaguchi K., Kinosaki M.,
RA   Mochizuki S.-I., Tomoyasu A., Yano K., Goto M., Murakami A., Tsuda E.,
RA   Morinaga T., Higashio K., Udagawa N., Takahashi N., Suda T.;
RT   "Osteoclast differentiation factor is a ligand for
RT   osteoprotegerin/osteoclastogenesis-inhibitory factor and is identical
RT   to TRANCE/RANKL.";
RL   Proc. Natl. Acad. Sci. U.S.A. 95:3597-3602(1998).
RN   [5]
RP   NUCLEOTIDE SEQUENCE (ISOFORM 1).
RC   STRAIN=129;
RX   MEDLINE=99214075; PubMed=10196481; DOI=10.1016/S0378-1119(99)00025-6;
RA   Kodaira K., Kodaira K., Mizuno A., Yasuda H., Shima N., Murakami A.,
RA   Ueda M., Higashio K.;
RT   "Cloning and characterization of the gene encoding mouse osteoclast
RT   differentiation factor.";
RL   Gene 230:121-127(1999).
RN   [6]
RP   NUCLEOTIDE SEQUENCE (ISOFORMS 1; 2 AND 3).
RX   MEDLINE=21150053; PubMed=11250921; DOI=10.1210/en.142.4.1419;
RA   Ikeda T., Kasai M., Utsuyama M., Hirokawa K.;
RT   "Determination of three isoforms of the receptor activator of nuclear
RT   factor-kappaB ligand and their differential expression in bone and
RT   thymus.";
RL   Endocrinology 142:1419-1426(2001).
RN   [7]
RP   PROTEIN SEQUENCE OF 139-147, PROCESSING, AND N-GLYCOSYLATION.
RX   MEDLINE=99240759; PubMed=10224132; DOI=10.1074/jbc.274.19.13613;
RA   Lum L., Wong B.R., Josien R., Becherer J.D., Erdjument-Bromage H.,
RA   Schloendorff J., Tempst P., Choi Y., Biobel C.P.;
RT   "Evidence for a role of a tumor necrosis factor-alpha (TNF-alpha)-
RT   converting enzyme-like protease in shedding of TRANCE, a TNF family
RT   member involved in osteoclastogenesis and dendritic cell survival.";
RL   J. Biol. Chem. 274:13613-13618(1999).
RN   [8]
RP   X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 158-316.
RX   MEDLINE=21464816; PubMed=11581298;
RA   Lam J., Nelson C.A., Ross F.P., Teitelbaum S.L., Fremont D.H.;
RT   "Crystal structure of the TRANCE/RANKL cytokine reveals determinants
RT   of receptor-ligand specificity.";
RL   J. Clin. Invest. 108:971-979(2001).
RN   [9]
RP   X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 137-316.
RX   MEDLINE=21839021; PubMed=11733492; DOI=10.1074/jbc.M10525200;
RA   Ito S., Wakabayashi K., Ubukata O., Hayashi S., Okada F., Hata T.;
RT   "Crystal structure of the extracellular domain of mouse RANK ligand at
RT   2.2-A resolution.";
RL   J. Biol. Chem. 277:6631-6636(2002).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to
CC       TNFRSF11A/RANK. Osteoclast differentiation and activation factor.
CC       Augments the ability of dendritic cells to stimulate naive T-cell
CC       proliferation. May be an important regulator of interactions
CC       between T cells and dendritic cells and may play a role in the
CC       regulation of the T cell-dependent immune response. May also play
CC       an important role in enhanced bone-resorption in humoral
CC       hypercalcemia of malignancy.
CC   -!- SUBUNIT: Homotrimer.
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted
CC       (isoforms 1 and 2); Cytoplasmic (isoform 3).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=3;
CC       Name=1;
CC         IsoId=O35235-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=O35235-2; Sequence=VSP_006449;
CC       Name=3;
CC         IsoId=O35235-3; Sequence=VSP_006448;
CC   -!- TISSUE SPECIFICITY: Highly expressed in thymus and lymph nodes,
CC       but not in nonlymphoid tissues and is abundantly expressed in T
CC       cells but not in B cells. A high level expression is also seen in
CC       the trabecular bone and lung.
CC   -!- PTM: N-glycosylated.
CC   -!- PTM: The soluble form of isoform 1 derives from the membrane form
CC       by proteolytic processing. The cleavage may be catalyzed by
CC       ADAM17. A further shorter soluble form was observed.
CC   -!- DISEASE: Deficiency in Tnfsf11 results in failure to form lobulo-
CC       alveolar mammary structures during pregnancy, resulting in death
CC       of newborns. Trance-deficient mice show severe osteopetrosis, with
CC       no osteoclasts, marrow spaces, or tooth eruption, and exhibit
CC       profound growth retardation at several skeletal sites, including
CC       the limbs, skull, and vertebrae and have marked chondrodysplasia,
CC       with thick, irregular growth plates and a relative increase in
CC       hypertrophic chondrocytes.
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
```

```
DR   EMBL; AF013170; AAC71061.1; -; mRNA.
DR   EMBL; AF019048; AAB86812.1; -; mRNA.
DR   EMBL; AF053713; AAC40113.1; -; mRNA.
DR   EMBL; AB008426; BAA25425.1; -; mRNA.
DR   EMBL; AB022039; BAA36970.1; -; Genomic_DNA.
DR   EMBL; AB032771; BAA97257.1; -; mRNA.
DR   EMBL; AB032772; BAA97258.1; -; mRNA.
DR   EMBL; AB036798; BAA97259.1; -; mRNA.
DR   PDB; 1IQA; X-ray; A/B/C=157-316.
DR   PDB; 1JTZ; X-ray; X/Y/Z=156-316.
DR   Ensembl; ENSMUSG00000022015; Mus musculus.
DR   MGI; MGI:1100089; Tnfsf11.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0045453; P:bone resorption; IDA.
DR   GO; GO:0007515; P:lymph gland development; IDA.
DR   GO; GO:0009887; P:organogenesis; TAS.
DR   GO; GO:0001503; P:ossification; IMP.
DR   GO; GO:0045672; P:positive regulation of osteoclast different. . .; IDA.
DR   GO; GO:0051260; P:protein homooligomerization; IDA.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM02207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; FALSE_NEG.
DR   PROSITE; PS50049; TNF_2; 1.
KW   3D-structure; Alternative splicing; Cytokine; Developmental protein;
KW   Differentiation; Direct protein sequencing; Glycoprotein; Receptor;
KW   Signal-anchor; Transmembrane.
FT   CHAIN         1    316       Tumor necrosis factor ligand superfamily
FT                                member 11, membrane form.
FT   CHAIN       139    316       Tumor necrosis factor ligand superfamily
FT                                member 11, soluble form.
FT   TOPO_DOM      1     48       Cytoplasmic (Potential).
FT   TRANSMEM     49     69       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM     70    316       Extracellular (Potential).
FT   SITE        138    139       Cleavage.
FT   CARBOHYD    197    197       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD    262    262       N-linked (GlcNAc...) (Potential).
FT   VARSPLIC      1    117       Missing (in isoform 3).
FT                                /FTId=VSP_006448.
FT   VARSPLIC     14     44       SSEEMGSSGPGVPHEGGPLHPAPSAPAPPPA -> TP (in
FT                                isoform 2).
FT                                /FTId=VSP_006449.
FT   CONFLICT     99     99       G -> D (in Ref. 2).
FT   CONFLICT    141    143       Missing (in Ref. 5).
FT   STRAND      164    169
FT   TURN        171    172
FT   STRAND      181    182
FT   STRAND      186    187
FT   TURN        191    192
FT   STRAND      194    196
FT   STRAND      198    201
```

OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: December 21, 2005, 12:35:06 ; Search time 18.5902 Seconds
1024.696 Million cell updates/sec
(without alignments)

Run on: US-09-211-297-32

Title:
Perfect score: 148
Sequence: 1 NAASIPSGSHKVTLSSWYHDRGWAKIS 27

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	148	100.0	316	1	TNF11_MOUSE	O35235 m tumor nec
2	140	94.6	318	1	TNF11_RAT	Q6ee2 r tumor nec
3	136	91.9	244	2	Q54A98_HUMAN	Q54a98 homo sapien
4	136	91.9	317	1	TNF11_HUMAN	O14788 h tumor nec
5	136	91.9	317	2	Q5T9Y4_HUMAN	Q5t9y4 homo sapien
6	136	91.9	317	2	Q5XLH0_RABIT	Q5xlh0 oryctolagus
7	88	59.5	117	2	Q6UWL7_HUMAN	Q6uwl7 homo sapien
8	76	51.4	95	2	Q6UY13_HUMAN	Q6uy13 homo sapien
9	76	51.4	95	2	Q9C4K2_9EURY	Q9c4k2 uncultured
10	61.5	41.6	456	1	MNTH_BRUME	P65544 brucella me
11	59	39.9	456	1	MNTH_BRUSU	P65545 brucella su
12	59	39.9	456	1	P65768_BRUAB	P57c68 brucella ab
13	59	39.9	157	2	Q9C4G1_9EURY	Q9c4g1 uncultured
14	59	39.9	157	2	Q9C4H5_9EURY	Q9c4h5 uncultured
15	58.5	39.5	157	2	Q9C4H7_9EURY	Q9c4h7 uncultured
16	58.5	39.5	157	2	Q9C4I3_9EURY	Q9c4i3 uncultured
17	58.5	39.5	157	2	Q9C4J1_9EURY	Q9c4j1 uncultured
18	58.5	39.5	157	2	Q7ZAE6_9EURY	Q7zae6 uncultured
19	58.5	39.5	163	2	Q8QOC2_METMA	Q8qoc2 methanosarc
20	58	39.2	371	2	Q41VP8_AZOVI	Q41vp8 azotobacter
21	57	38.5	255	2	Q9C4G6_9EURY	Q9c4g6 uncultured
22	56.5	38.2	157	2	Q9C4I8_9EURY	Q9c4i8 uncultured
23	56.5	38.2	162	2	Q6SEI7_9EURY	Q6sei7 uncultured
24	56.5	38.2	211	2	Q75NC5_9ARCH	Q75nc5 uncultured
25	56.5	38.2	224	2	Q6VF0_9ARCH	Q6vf0 uncultured
26	56.5	38.2	235	2	Q6VF2_9ARCH	Q6vf2 uncultured
27	56.5	38.2	235	2	Q6VF3_9ARCH	Q6vf3 uncultured
28	56.5	38.2	235	2	Q6VF5_9ARCH	Q6vf5 uncultured
29	56.5	38.2	235	2	Q6VF8_9ARCH	Q6vf8 uncultured
30	56.5	38.2	235	2	Q5EGK0_9EURY	Q5egk0 uncultured
31	56.5	38.2	235	2	Q5EGK6_9EURY	Q5egk6 uncultured
32	56.5	38.2	254	2	Q5EGK5_9EURY	Q5egk5 uncultured
33	56.5	38.2	254	2	Q5EGJ9_9EURY	Q5egj9 uncultured
34	56.5	38.2	561	2	Q64C70_9ARCH	Q64c70 uncultured
35	56	37.8	334	2	Q7NRU9_CHRVO	Q7nru9 chromobacte
36	56	37.8	756	2	Q4IZG3_AZOVI	Q4izg3 azotobacter
37	55.5	37.5	162	2	Q6JI92_9EURY	Q6ji92 uncultured
38	55.5	37.5	224	2	Q6VVE9_9ARCH	Q6vve9 uncultured
39	55.5	37.5	254	2	Q5EGJ8_9EURY	Q5egj8 uncultured
40	55.5	37.5	254	2	Q5EGJ6_9EURY	Q5egj6 uncultured
41	55.5	37.5	561	2	Q648Y3_9ARCH	Q648y3 uncultured
42	55	37.2	606	2	Q6VUA1_9ARCH	Q6vua1 uncultured
43	54.5	36.8	156	2	Q4TR89_9SPHN	Q4tr89 erythrobact
44	54.5	36.8	157	2	Q6ZXA8_9EURY	Q6zxa8 uncultured
45	54.5	36.8	254	2	Q9C4H0_9EURY	Q9c4h0 uncultured

ALIGNMENTS

RESULT 1
TNF11_MOUSE

```
ID   TNF11_MOUSE              STANDARD;      PRT;   316 AA.
AC   O35235; O35306; Q9JJK8; Q9JJK9; Q9RIY0;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Tumor necrosis factor ligand superfamily member 11 (Receptor activator
DE   of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-
DE   induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast
DE   differentiation factor) (ODF) [Contains: Tumor necrosis factor ligand
DE   superfamily member 11, membrane form; Tumor necrosis factor ligand
DE   superfamily member 11, soluble form].
GN   Name=Tnfsf11; Synonyms=Opgl, Rankl, Trance;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE (ISOFORM 1).
RC   TISSUE=Hybridoma;
RX   MEDLINE=97460112; PubMed=9312132; DOI=10.1074/jbc.272.40.25190;
RA   Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M.,
RA   Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
RA   Choi Y.;
RT   "TRANCE is a novel ligand of the tumor necrosis factor receptor family
RT   that activates c-Jun N-terminal kinase in T cells.";
RL   J. Biol. Chem. 272:25190-25194(1997).
RN   [2]
RP   NUCLEOTIDE SEQUENCE (ISOFORM 1).
RP   TISSUE=Thymic lymphoma;
RX   MEDLINE=98032977; PubMed=9367155; DOI=10.1038/36593;
RA   Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
RA   Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
RA   Galibert L.;
RT   "A homologue of the TNF receptor and its ligand enhance T-cell growth
RT   and dendritic-cell function.";
RL   Nature 390:175-179(1997).
RN   [3]
RP   NUCLEOTIDE SEQUENCE (ISOFORM 1).
RC   TISSUE=Bone marrow;
RX   MEDLINE=98227661; PubMed=9568710; DOI=10.1016/S0092-8674(00)81569-X;
RA   Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,
RA   Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,
RA   Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,
RA   Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,
RA   Boyle W.J.;
RT   "Osteoprotegerin ligand is a cytokine that regulates osteoclast
RT   differentiation and activation.";
RL   Cell 93:165-176(1998).
RN   [4]
RP   NUCLEOTIDE SEQUENCE (ISOFORM 1).
RC   TISSUE=Bone marrow stroma;
```

```
RX   MEDLINE=98188248; PubMed=9520411; DOI=10.1073/pnas.95.7.3597;
RA   Yasuda H., Shima N., Nakagawa N., Yamaguchi K., Kinosaki M.,
RA   Mochizuki S.-I., Tomoyasu A., Yano K., Goto M., Murakami A., Tsuda E.,
RA   Morinaga T., Higashio K., Udagawa N., Takahashi N., Suda T.;
RT   "Osteoclast differentiation factor is a ligand for
RT   osteoprotegerin/osteoclastogenesis-inhibitory factor and is identical
RT   to TRANCE/RANKL.";
RL   Proc. Natl. Acad. Sci. U.S.A. 95:3597-3602(1998).
RN   [5]
RP   NUCLEOTIDE SEQUENCE (ISOFORM 1).
RC   STRAIN=129;
RX   MEDLINE=99216075; PubMed=9921075; DOI=10.1016/S0378-1119(99)00025-6;
RA   Kodaira K., Kodaira K., Mizuno A., Yasuda H., Shima N., Murakami A.,
RA   Ueda M., Higashio K.;
RT   "Cloning and characterization of the gene encoding mouse osteoclast
RT   differentiation factor.";
RL   Gene 230:121-127(1999).
RN   [6]
RP   NUCLEOTIDE SEQUENCE (ISOFORMS 1, 2 AND 3).
RX   MEDLINE=21150053; PubMed=11250921; DOI=10.1210/en.142.4.1419;
RA   Ikeda T., Kasai M., Utsuyama M., Hirokawa K.;
RT   "Determination of three isoforms of the receptor activator of nuclear
RT   factor-kappaB ligand and their differential expression in bone and
RT   thymus.";
RL   Endocrinology 142:1419-1426(2001).
RN   [7]
RP   PROTEIN SEQUENCE OF 139-147, PROCESSING, AND N-GLYCOSYLATION.
RX   MEDLINE=99240759; PubMed=10224132; DOI=10.1074/jbc.274.19.13613;
RA   Schlondorff J., Tempst P., Choi Y., Biobel C.P.;
RT   "Evidence for a role of a tumor necrosis factor-alpha (TNF-alpha)-
RT   converting enzyme-like protease in shedding of TRANCE, a TNF family
RT   member involved in osteoclastogenesis and dendritic cell survival.";
RL   J. Biol. Chem. 274:13613-13618(1999).
RN   [8]
RP   X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 158-316.
RX   MEDLINE=21464816; PubMed=11581298;
RA   Lam J., Nelson C.A., Ross F.P., Teitelbaum S.L., Fremont D.H.;
RT   "Crystal structure of the TRANCE/RANKL cytokine reveals determinants
RT   of receptor-ligand specificity.";
RL   J. Clin. Invest. 108:971-979(2001).
RN   [9]
RP   X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 137-316.
RX   MEDLINE=21839021; PubMed=11733492; DOI=10.1074/jbc.M10652520O;
RA   Ito S., Wakabayashi K., Ubukata O., Hayashi S., Okada F., Hata T.;
RT   "Crystal structure of the extracellular domain of mouse RANK ligand at
RT   2.2-A resolution.";
RL   J. Biol. Chem. 277:6631-6636(2002).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to
CC       TNFRSF11A/RANK. Osteoclast differentiation and activation factor.
CC       Augments the ability of dendritic cells to stimulate naive T-cell
CC       proliferation. May be an important regulator of interactions
CC       between T cells and dendritic cells and may play a role in the
CC       regulation of the T cell-dependent immune response. May also play
CC       an important role in enhanced bone-resorption in humoral
CC       hypercalcemia of malignancy.
CC   -!- SUBUNIT: Homotrimer.
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted
CC       (isoforms 1 and 2). Cytoplasmic (isoform 3).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=3;
CC       Name=1;
CC         IsoId=O35235-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=O35235-2; Sequence=VSP_006449;
CC       Name=3;
CC         IsoId=O35235-3; Sequence=VSP_006448;
CC   -!- TISSUE SPECIFICITY: Highly expressed in thymus and lymph nodes,
CC       but not in nonlymphoid tissues and is abundantly expressed in T
CC       cells but not in B cells. A high level expression is also seen in
CC       the trabecular bone and lung.
CC   -!- PTM: N-glycosylated.
CC   -!- PTM: The soluble form of isoform 1 derives from the membrane form

CC       by proteolytic processing. The cleavage may be catalyzed by
CC       ADAM17. A further shorter soluble form was observed.
CC   -!- DISEASE: Deficiency in Tnfsf11 results in failure to form lobulo-
CC       alveolar mammary structures during pregnancy, resulting in death
CC       of newborns. Trance-deficient mice show severe osteopetrosis, with
CC       no osteoclasts, marrow spaces, or tooth eruption, and exhibit
CC       profound growth retardation at several skeletal sites, including
CC       the limbs, skull, and vertebrae and have marked chondrodysplasia,
CC       with thick, irregular growth plates and a relative increase in
CC       hypertrophic chondrocytes.
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------------
DR   EMBL; AF013170; AAC71061.1; -; mRNA.
DR   EMBL; AF019048; AAB86812.1; -; mRNA.
DR   EMBL; AF053713; AAC40113.1; -; mRNA.
DR   EMBL; AB008426; BAA25425.1; -; mRNA.
DR   EMBL; AB022039; BAA36970.1; -; Genomic_DNA.
DR   EMBL; AB032771; BAA97257.1; -; mRNA.
DR   EMBL; AB032772; BAA97258.1; -; mRNA.
DR   EMBL; AB036798; BAA97259.1; -; mRNA.
DR   PDB; 1IQA; X-ray; A/B/C=157-316.
DR   PDB; 1JTZ; X-ray; X/Y/Z=156-316.
DR   MGI; MGI:1100089; Tnfsf11.
DR   Ensembl; ENSMUSG00000022015; Mus musculus.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; FALSE_NEG.
DR   PROSITE; PS50049; TNF_2; 1.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0045453; P:bone resorption; IDA.
DR   GO; GO:0007515; P:lymph gland development; IDA.
DR   GO; GO:0009887; P:organogenesis; IMP.
DR   GO; GO:0001503; P:ossification; IMP.
DR   GO; GO:0045672; P:positive regulation of osteoclast different... .; IDA.
DR   GO; GO:0051260; P:protein homooligomerization; IDA.
KW   3D-structure; Alternative splicing; Cytokine; Developmental protein;
KW   Differentiation; Direct protein sequencing; Glycoprotein; Receptor;
KW   Signal-anchor; Transmembrane.
FT   CHAIN         1    316       Tumor necrosis factor ligand superfamily
FT                                member 11, membrane form.
FT   CHAIN       139    316       Tumor necrosis factor ligand superfamily
FT                                member 11, soluble form.
FT   TOPO_DOM      1     48       Cytoplasmic (Potential).
FT   TRANSMEM     49     69       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM     70    316       Extracellular (Potential).
FT   SITE        138    139       Cleavage.
FT   CARBOHYD    197    197       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD    262    262       N-linked (GlcNAc...) (Potential).
FT   VARSPLIC      1    117       Missing (in isoform 3).
FT                                /FTId=VSP_006448.
FT   VARSPLIC     14     44       SSEEMSGSGPGVPHEGPLHPAPSAPAPAPPPA -> TP (in
FT                                isoform 2).
FT                                /FTId=VSP_006449.
FT   CONFLICT     99     99       G -> D (in Ref. 2).
FT   CONFLICT    141    143       Missing (in Ref. 5).
FT   STRAND      164    169
FT   TURN        171    172
FT   STRAND      181    182
FT   STRAND      186    187
FT   TURN        191    191
FT   STRAND      191    192
FT   TURN        194    196
FT   STRAND      198    201
```

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OM protein - protein search, using sw model

Run on: December 21, 2005, 12:34:10 ; Search time 18.3689 Seconds
(without alignments)
645.834 Million cell updates/sec

Title: US-09-211-297-32
Perfect score: 148
Sequence: 1 NAASIPSGSHKVTLSSWYHDRGWAKIS 27
Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	148	100.0	27	2	AAW83196	Aaw83196 Murine os
2	148	100.0	28	2	AAW83197	Aaw83197 Murine os
3	148	100.0	155	6	ABR39854	Abr39854 RANK liga
4	148	100.0	155	7	ADC03334	Adc03334 Murine re
5	148	100.0	155	7	ADI53055	Adi53055 Human RAN
6	148	100.0	160	3	AAB08272	Aab08272 Amino aci
7	148	100.0	170	4	AAU08386	Aau08386 Mouse FLA
8	148	100.0	170	3	ADJ82132	Adj82132 Protein f
9	148	100.0	173	3	AAY84426	Aay84426 An osteop
10	148	100.0	173	3	AAY84422	Aay84422 A murine
11	148	100.0	173	3	AAY84425	Aay84425 DNA encod
12	148	100.0	173	3	AAY84421	Aay84421 Amino aci
13	148	100.0	182	3	AAY84424	Aay84424 An osteop
14	148	100.0	187	3	AAY84420	Aay84420 Amino aci
15	148	100.0	188	3	AAY84423	Aay84423 An osteop
16	148	100.0	193	7	ADJ82129	Adj82129 Protein f
17	148	100.0	199	5	ABG94285	Abg94285 Mouse RAN
18	148	100.0	199	5	ABG80597	Abg80597 Mouse rec
19	148	100.0	199	7	ADJ82119	Adj82119 Protein f
20	148	100.0	216	7	ADB16999	Adb16999 Murine RA
21	148	100.0	244	2	AAW83019	Aaw83019 A murine
22	148	100.0	247	5	ABG94284	Abg94284 Mouse RAN
23	148	100.0	247	5	ABG80596	Abg80596 Mouse rec
24	148	100.0	247	7	ADJ82118	Adj82118 Protein f
25	148	100.0	249	6	ADA50081	Ada50081 Mouse wil
26	148	100.0	294	2	AAW69956	Aaw69956 NF-kB rec
27	148	100.0	294	2	AAW68292	Aaw68292 NF-kB rec
28	148	100.0	294	2	AAE08737	Aae08737 Murine re
29	148	100.0	294	4	AAE04425	Aae04425 Murine re
30	148	100.0	294	4	AAE01992	Aae01992 Murine RA
31	148	100.0	294	5	AAE26102	Aae26102 Mouse RAN
32	148	100.0	294	5	ADB16986	Adb16986 Murine re
33	148	100.0	294	7	ADC73000	Adc73000 Murine RA
34	148	100.0	294	7	ADC78266	Adc78266 Murine RA
35	148	100.0	294	7	ADG46721	Adg46721 Murine RA
36	148	100.0	294	9	ADW09027	Adw09027 Murine re
37	148	100.0	316	2	AAW83017	Aaw83017 Osteoclas
38	148	100.0	316	2	AAW83194	Aaw83194 Human ost
39	148	100.0	316	2	AAW59654	Aaw59654 Amino aci
40	148	100.0	316	2	AAY17874	Aay17874 Murine TR
41	148	100.0	316	3	AAY91024	Aay91024 Mouse OBM
42	148	100.0	316	3	AAY84418	Aay84418 Amino aci
43	148	100.0	316	3	AAY84419	Aay84419 Amino aci
44	148	100.0	316	5	AAU78289	Aau78289 Mouse TRA
45	148	100.0	316	5	ADR29338	Adr29338 Mouse RAN

ALIGNMENTS

RESULT 1
AAW83196
ID AAW83196 standard; peptide; 27 AA.
XX
AC AAW83196;
XX
DT 11-FEB-1999 (first entry)
XX
DE Murine osteoprotegerin binding protein BB' loop peptide.
XX
KW Osteoprotegerin binding protein; OPG binding protein; arthritis;
KW osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR;
KW hypercalcaemia; osteoclast differentiation and activation receptor;
KW Paget's disease.
XX
OS Mus sp.
XX
XX
PN WO9846751-A1.
XX
PD 22-OCT-1998.
XX
XX
PF 15-APR-1998; 98WO-US007584.
XX
PR 16-APR-1997; 97US-00842842.
PR 23-JUN-1997; 97US-00880855.
PR 30-MAR-1998; 98US-00052521.
XX
PA (AMGE-) AMGEN INC.
XX
PI Boyle WJ;
XX
PT WPI; 1998-594578/50.
DR
XX
PT Nucleic acid encoding osteoprotegerin binding protein - useful for, e.g.
PT treating bone diseases by modulating osteoclast differentiation and for
PT diagnosis.
XX
PS Example 11; Page 55; 47pp; English.
XX
CC The present sequence represents peptide from murine osteoprotegerin (OPG)
CC binding protein. Host cells transfected with vectors containing nucleic
CC acid molecules encoding OPG binding protein are used to produce
CC recombinant OPG binding protein. OPG binding protein is used in binding
CC assays to determine osteoprotegerin (OG) in biological samples; to screen
CC for specific binding agents (particularly agonists and antagonists,
CC including intracellular proteins); to raise Ab (useful in immunoassays
CC for detection of OPG binding protein) and to identify compounds that

RESULT 2
AAW83197

ID   AAW83197 standard; peptide; 28 AA.
XX
AC   AAW83197;
XX
DT   11-FEB-1999 (first entry)
XX
DE   Murine osteoprotegerin binding protein BB' loop-Cys peptide.
XX
KW   Osteoprotegerin binding protein; OPG binding protein; arthritis;
KW   osteoporosis; osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR;
KW   hypercalcaemia; osteoclast differentiation and activation receptor;
KW   Paget's disease.
XX
OS   Mus sp.
XX
PN   WO9846751-A1.
XX
PD   22-OCT-1998.
XX
PF   15-APR-1998;
PD   15-APR-1998;   98WO-US007584.
PR   16-APR-1997;   97US-00842842.
PR   23-JUN-1997;   97US-00880855.
PR   30-MAR-1998;   98US-00052521.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Boyle WJ;
XX
DR   WPI; 1998-594578/50.
XX
PT   Nucleic acid encoding osteoprotegerin binding protein - useful for, e.g.
PT   treating bone diseases by modulating osteoclast differentiation and for
PT   diagnosis.
XX
PS   Example 11; Page 55; 47pp; English.
XX
CC   The present sequence represents peptide from murine osteoprotegerin (OPG)
CC   binding protein. Host cells transfected with vectors containing nucleic
CC   acid molecules encoding OPG binding protein are used to produce
CC   recombinant OPG binding protein. OPG binding protein is used in binding
CC   assays to determine osteoprotegerin (OG) in biological samples; to screen
CC   for specific binding agents (particularly agonists and antagonists,
CC   including intracellular proteins); to raise Ab (useful in immunoassay
CC   for detection of OPG binding protein) and to identify compounds that
CC   modulate binding of OPG binding protein to osteoclast differentiation and
CC   activation receptor (ODAR). The nucleic acid molecule encoding OPG
CC   binding protein can be used to detect OPG binding protein-encoding
CC   sequences, e.g. screening for related sequences, also to produce
CC   transgenic animal models while complementary sequences are used for
CC   antisense regulation of OPG binding protein expression. Modulators of OPG
CC   binding protein, particularly soluble forms of OPG binding protein or Ab,
CC   are used to treat or prevent bone diseases, e.g. osteoporosis, bone loss
CC   caused by arthritis or metastases, hypercalcaemia, Paget's disease,
CC   periodontal disease, osteoporosis, loosening of prostheses, optionally in
CC   combination with agents that promote bone growth
XX
SQ   Sequence 27 AA;

Qy
Db

Query Match   100.0%; Score 148; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 7.8e-16;
Matches   27; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 NAASIPSGSHKVTLSSWYHDRGWAKIS 27
         |||||||||||||||||||||||||||
Db   1 NAASIPSGSHKVTLSSWYHDRGWAKIS 27

CC   sequences, e.g. screening for related sequences, also to produce
CC   transgenic animal models, while complementary sequences are used for
CC   antisense regulation of OPG binding protein expression. Modulators of OPG
CC   binding protein, particularly soluble forms of OPG binding protein or Ab,
CC   are used to treat or prevent bone diseases, e.g. osteoporosis, bone loss
CC   caused by arthritis or metastases, hypercalcaemia, Paget's disease,
CC   periodontal disease, osteoporosis, loosening of prostheses, optionally in
CC   combination with agents that promote bone growth
XX
SQ   Sequence 28 AA;

Qy
Db

Query Match   100.0%; Score 148; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 8.1e-16;
Matches   27; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 NAASIPSGSHKVTLSSWYHDRGWAKIS 27
         |||||||||||||||||||||||||||
Db   1 NAASIPSGSHKVTLSSWYHDRGWAKIS 27

RESULT 3
ABR39854

ID   ABR39854 standard; protein; 155 AA.
XX
AC   ABR39854;
XX
DT   11-AUG-2003 (first entry)
XX
DE   RANK ligand (RANKL) protein fragment.
XX
KW   RANK; receptor activator of necrosis factor kB; RANK ligand; RANKL;
KW   mouse.
XX
OS   Mus sp.
XX
PN   WO200301407?-A2.
XX
PD   20-FEB-2003.
XX
PF   09-AUG-2002; 2002WO-US025287.
PR   09-AUG-2001; 2001US-0311163P.
PR   22-MAR-2002; 2002US-00105057.
XX
PA   (BARN-) BARNES-JEWISH HOSPITAL.
XX
PI   Lam J, Ross FP, Teitelbaum SL, Nelson CA, Fremont DH;
XX
DR   WPI; 2003-256526/25.
XX
PT   Composition for identifying a compound with Receptor Activator of
PT   Necrosis Factor kB, RANK modulating activity and for identifying RANK or
PT   osteoprotegerin modulating compound, has a protein complex in crystalline
PT   form.
XX
PS   Disclosure; Fig 3; 66pp; English.
XX
CC   The invention relates to a composition (I) comprising a protein complex
CC   in crystalline form, where the complex comprises an amino acid sequence
CC   of a Receptor Activator of Necrosis Factor kB (RANK) Ligand (RANKL)
CC   ectodomain. (I) is useful for identifying a compound with RANK modulating
CC   activity, and for identifying a RANK or OPG modulating compound. (I) is
CC   useful to intelligently design mutants that have altered biological
CC   properties and for identifying and/or designing compounds that bind RANK
CC   as an approach towards developing new therapeutic agents. (I) is also
CC   useful to computationally screen small molecule databases for chemical
CC   entities or compounds that can bind in whole, or in part, to RANK or
CC   RANKL. The present sequence represents a murine RANKL protein fragment
XX
SQ   Sequence 155 AA;

Qy
Db

Query Match   100.0%; Score 148; DB 6; Length 155;
Best Local Similarity 100.0%; Pred. No. 6.6e-15;

OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: December 21, 2005, 12:47:51 ; Search time 3.0541 Seconds
(without alignments)
850.612 Million cell updates/sec

Scoring table: Sequence: 1 NAASIPSGSHKVTLSSWYHDRGWAKIS 27
Perfect score: 148
Title:

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 9621763 residues

Total number of hits satisfying chosen parameters: 283416

Maximum DB seq length: 2000000000
Minimum DB seq length: 0

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Databases :
PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	59	39.9	456	2	AC3323	manganese transpor
2	49	33.1	369	2	C97484	outer membrane pro
3	49	33.1	369	2	AC2702	outer membrane pro
4	49	33.1	417	2	A96610	probable pectinace
5	49	33.1	747	2	F87263	TPR domain protein
6	49	33.1	780	2	G72724	probable penicilli
7	49	33.1	827	1	A36895	endopeptidase La (
8	48.5	32.8	199	2	AD2486	hypothetical prote
9	48.5	32.8	570	2	E29525	methyl coenzyme M
10	48	32.4	245	2	B86889	zinc ABC transport
11	48	32.4	452	2	E84186	hypothetical prote
12	48	32.4	831	2	T00323	chitinase (EC 3.2.
13	48	32.4	1888	2	T39009	hypothetical prote
14	47.5	32.1	197	2	B96568	hypothetical prote
15	47.5	32.1	230	2	A96565	hypothetical prote
16	47	31.8	398	2	I49443	gene 2B4 protein -
17	47	31.8	406	2	AG0548	probable ABC-trans
18	47	31.8	442	2	T50687	proline transport
19	47	31.8	442	2	S42864	protein kinase (EC
20	47	31.8	522	2	D96836	probable glycerol
21	47	31.8	576	2	A53982	capsid protein - E
22	47	31.8	593	2	A41617	dopamine transport
23	47	31.8	1520	2	T30820	carbamoyl-phosphat
24	46.5	31.4	172	2	E96518	protein T2E6.12 [i
25	46.5	31.4	197	2	A96568	hypothetical prote
26	46.5	31.4	637	2	S01509	NADH2 dehydrogenas
27	46	31.1	336	2	F84056	hypothetical prote
28	46	31.1	336	2	F95925	probable cell-wall
29	46	31.1	350	2	T32215	hypothetical prote
30	46	31.1	394	1	S77216	hypothetical prote
31	46	31.1	512	2	A54400	protein kinase (EC
32	46	31.1	605	1	Q0B83R	BVRF2 (EC-RF3) pro
33	46	31.1	686	2	T15795	hypothetical prote
34	45.5	30.7	263	2	AD0851	secretory protein
35	45.5	30.7	756	1	AI3275	phosphoenolpyruvat
36	45	30.4	105	2	T38761	hypothetical prote
37	45	30.4	112	2	E83817	hypothetical prote
38	45	30.4	205	2	A75165	thymidylate kinase
39	45	30.4	205	2	C43670	integral membrane
40	45	30.4	288	2	A05062	probable mbpY prot
41	45	30.4	325	2	S58146	hypothetical prote
42	45	30.4	334	2	T40042	conserved hypothet
43	45	30.4	345	2	F90194	threonine synthase
44	45	30.4	365	2	AE2782	transcription regu
45	45	30.4	365	2	F97561	hypothetical prote

ALIGNMENTS

RESULT 1
AC3323
manganese transport protein mntH [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AC3323
R;Delvecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Reference number: AD3252; PMID:11756688
A;Accession: AC3323
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-456 <KUR>
A;Cross-references: UNIPROT:Q8YI76; UNIPARC:UPI00000057D23; GB:AE008917; PIDN:AAL51750.1;
A;Experimental source: strain 16M
A;Accession: AC3323
C;Genetics:
A;Gene: BME10569
A;Map position: I
C;Superfamily: natural resistance-associated macrophage protein 1

Query Match   39.9%; Score 59; DB 2; Length 456;
Best Local Similarity   45.8%;
Matches   11; Conservative   4; Mismatches   9; Indels   0; Gaps   0;

Qy   4 SIPGGSHKVTLSSWYHDRGWAKIS 27
            |||| ::||::|| :|||:|||::|
Db   6 SCPSGAREVTFEGWRRERGEASMS 29

RESULT 2
C97484
outer membrane protein a2 precursor [imported] - Agrobacterium tumefaciens (strain C58,
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: C97484
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: C97484
A;Status: preliminary
A;Molecule type: DNA
A;Residue: 1-369 <KUR>
A;Cross-references: UNIPROT:Q8UGL7; UNIPARC:UPI00000D19FA; GB:AE007869; PIDN:AAK86828.1;
C;Genetics:
A;Gene: AGR_C_1878
A;Map position: circular chromosome

Query Match   33.1%; Score 49; DB 2; Length 369;

RESULT 3

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Qy        1 NAASIPSGSHKVTLSSWYHDRGW 23
            ||| | || :| : | ||
Db      305 NAAGVPTGASAIITNDWSNRDAW 327
```

Best Local Similarity 30.4%; Pred. No. 22;
Matches 7; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

AC2702
A;Accession: AC2702
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-369 <KUR>
A;Cross-references: UNIPROT:Q8UGL7; UNIPARC:UPI00000D19FA; GB:AE008688; PIDN:AAL42033.1;
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu1020
A;Map position: circular chromosome

RESULT 4

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Qy        1 NAASIPSGSHKVTLSSWYHDRGW 23
            ||| | || :| : | ||
Db      305 NAAGVPTGASAIITNDWSNRDAW 327
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Best Local Similarity 30.4%; Pred. No. 22;
Matches 7; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

A96610
A;Accession: A96610
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-417 <STO>
A;Cross-references: UNIPROT:Q9FVU3; UNIPARC:UPI000004831; GB:AE005173; NID:g11055858; F
C;Genetics:

probable pectinacetylesterase precursor T8L23.6 [imported] - Arabidopsis thaliana
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, W.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: A96610
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-417 <STO>
A;Cross-references: UNIPROT:Q9FVU3; UNIPARC:UPI000004831; GB:AE005173; NID:g11055858; F
C;Genetics:
A;Gene: T8L23.6
A;Map position: 1

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Qy        1 NAASIPSGSHKVTLSSWYHDRGWAKI 26
            :| :| |
Db
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Query Match   Score 49; DB 2; Length 417;
Best Local Similarity 34.6%; Pred. No. 25;
Matches 9; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

Db   374 NSPAIRNKGIAVAVGDWYFERGGAKL 399

RESULT 5

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Qy        1 NAASIPSGSHKVTLSSWYHDRGW 23
            |||| | |||  || |  |  |
Db      138 NLAAAESQAHALTLSFPNHELGW 160
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Query Match   Score 49; DB 2; Length 747;
Best Local Similarity 43.5%; Pred. No. 46;
Matches 10; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

F87263
A;Accession: F87263
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
TPR domain protein [imported] - Caulobacter crescentus
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolona
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-747 <STO>
A;Cross-references: UNIPROT:Q9ABV1; UNIPARC:UPI00000C6F34; GB:AE005673; NID:g13421226; P
C;Genetics:
A;Gene: CC0119

RESULT 6

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Qy        1 NAASIPSGSHKVTLSSWYHDRGW 23
            || :|: | : | :| |||
Db      160 NLAAAESQAHALTLSFPNHELGW 160
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Query Match   Score 49; DB 2; Length 780;
Best Local Similarity 50.0%; Pred. No. 48;
Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

G72724
A;Accession: G72724
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
probable penicillin acylase APE0336 - Aeropyrum pernix (strain K1)
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takaha
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Ka
DNA Res. 6, 83-101, 1999
A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-780 <KAW>
A;Cross-references: UNIPROT:Q9YFA5; UNIPARC:UPI00000SDAD8; DDBJ:AP000059; NID:g95103911;
A;Experimental source: strain K1
C;Genetics:
A;Gene: APE0336

RESULT 7

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Qy        4 SIPSGSHKVTLSSWYHDRGW 23
            || :|| ||| |||  |
Db      734 SLPGGSSGVPLSSFYDNLYW 753
```

A36895
A;Accession: A36895; A36894
C;Species: Myxococcus xanthus
C;Date: 09-Apr-1999 #sequence_revision 09-Apr-1999 #text_change 09-Jul-2004
endopeptidase La (EC 3.4.21.53) 2 - Myxococcus xanthus
N;Alternate names: ATP-dependent proteinase BsgA; ATP-dependent protease lonD; ATP-depe
N;Contains: adenosinetriphosphatase (EC 3.6.1.3)
R;Tojo, N.; Inouye, S.; Komano, T.
J. Bacteriol. 175, 4545-4549, 1993
A;Reference number: A36895; MUID:93322335; PMID:8331083
A;Title: The lonD gene is homologous to the lon gene encoding an ATP-dependent protease

OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: December 21, 2005, 12:44:31 ; Search time 4.60328 seconds
                                                          (without alignments)
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Title: US-09-211-297-32
Perfect score: 148
Sequence: 1 NAASIPSGSHKVTLSSWYHDRGWAKIS 27

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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                4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
                6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	148	100.0	28	2	US-09-052-521C-34	Sequence 34, Appli
2	148	100.0	77	2	US-09-632-287A-10	Sequence 10, Appl
3	148	100.0	77	2	US-10-286-696-10	Sequence 10, Appl
4	148	100.0	173	2	US-09-396-937-12	Sequence 12, Appl
5	148	100.0	173	2	US-09-396-937-18	Sequence 18, Appl
6	148	100.0	173	2	US-09-396-937-20	Sequence 20, Appl
7	148	100.0	173	2	US-09-396-937-16	Sequence 16, Appl
8	148	100.0	182	2	US-09-052-521C-4	Sequence 4, Appli
9	148	100.0	187	2	US-09-396-937-8	Sequence 8, Appli
10	148	100.0	188	2	US-09-396-937-14	Sequence 14, Appl
11	148	100.0	294	2	US-08-996-139-11	Sequence 11, Appl
12	148	100.0	294	2	US-08-995-659-11	Sequence 11, Appl
13	148	100.0	294	2	US-09-215-649A-11	Sequence 11, Appl
14	148	100.0	294	2	US-09-577-780-11	Sequence 11, Appl
15	148	100.0	294	2	US-09-577-800-11	Sequence 11, Appl
16	148	100.0	294	2	US-09-466-496-11	Sequence 11, Appl
17	148	100.0	294	2	US-09-871-856-11	Sequence 11, Appl
18	148	100.0	294	2	US-09-871-291-11	Sequence 11, Appl
19	148	100.0	294	2	US-09-877-650-11	Sequence 11, Appl
20	148	100.0	294	2	US-09-865-363-11	Sequence 11, Appl
21	148	100.0	294	2	US-09-688-459-11	Sequence 11, Appl
22	148	100.0	294	1	US-08-842-842-7	Sequence 7, Appl
23	148	100.0	294	2	US-08-989-362-7	Sequence 7, Appl
24	148	100.0	316	2	US-09-052-521C-2	Sequence 2, Appli
25	148	100.0	316	2	US-09-671-658A-2	Sequence 2, Appli
26	148	100.0	316	2	US-09-396-937-4	Sequence 4, Appli
27	148	100.0	316	2	US-09-396-937-6	Sequence 6, Appli
28	148	100.0	316	2	US-09-957-944-8	Sequence 8, Appli
29	136	91.9	77	2	US-09-632-287A-11	Sequence 11, Appl
30	136	91.9	77	2	US-10-286-696-11	Sequence 11, Appl
31	136	91.9	317	2	US-08-996-139-13	Sequence 13, Appl
32	136	91.9	317	2	US-08-995-659-13	Sequence 13, Appl
33	136	91.9	317	2	US-09-215-649A-13	Sequence 13, Appl
34	136	91.9	317	2	US-09-052-521C-4	Sequence 4, Appli
35	136	91.9	317	2	US-09-577-780-13	Sequence 13, Appl
36	136	91.9	317	2	US-09-577-800-13	Sequence 13, Appl
37	136	91.9	317	2	US-09-466-496-13	Sequence 13, Appl
38	136	91.9	317	2	US-09-871-856-13	Sequence 13, Appl
39	136	91.9	317	2	US-09-871-291-13	Sequence 13, Appl
40	136	91.9	317	2	US-09-877-650-13	Sequence 13, Appl
41	136	91.9	317	2	US-09-865-363-13	Sequence 13, Appl
42	136	91.9	317	2	US-09-688-459-13	Sequence 13, Appl
43	136	91.9	317	2	US-09-957-944-6	Sequence 6, Appli
44	136	91.9	317	2	US-09-052-521C-33	Sequence 33, Appl
45	135	91.2	27	2	US-09-052-521C-33	Sequence 33, Appl

ALIGNMENTS

RESULT 1
US-09-052-521C-34
; Sequence 34, Application US/09052521C
; Patent No. 6316408
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors
; FILE REFERENCE: A-451Brv
; CURRENT APPLICATION NUMBER: US/09/052,521C
; CURRENT FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 08/880,855
; PRIOR FILING DATE: 1997-06-23
; PRIOR APPLICATION NUMBER: 08/842,842
; PRIOR FILING DATE: 1997-04-16
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 34
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Oligonucleotide
US-09-052-521C-34

Query Match   100.0%; Score 148; DB 2; Length 28;
Best Local Similarity   100.0%; Pred. No. 5.5e-15;
Matches   27; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Db   1 NAASIPSGSHKVTLSSWYHDRGWAKIS 27

RESULT 2
US-09-632-287A-10
; Sequence 10, Application US/09632287A
; Patent No. 6521422
; GENERAL INFORMATION:
; APPLICANT: Hsu, Hailing
; APPLICANT: Wooden, Scott K
; APPLICANT: Boyle, William J
; TITLE OF INVENTION: Fhm, A No. 6521422el Member of the TNF Ligand Supergene Family
; FILE REFERENCE: 01017/35550A
; CURRENT APPLICATION NUMBER: US/09/632,287A
; CURRENT FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/147,294
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 10
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Mouse
US-09-632-287A-10

Qy   1 NAASIPSGSHKVTLSSWYHDRGWAKIS 27
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Db   14 NAASIPSGSHKVTLSSWYHDRGWAKIS 40

Query Match   100.0%; Score 148; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 1.9e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
US-10-286-696-10
; Sequence 10, Application US/10286696
; Patent No. 6852839
; GENERAL INFORMATION:
; APPLICANT: Heu, Hailing
; APPLICANT: Wooden, Scott K
; APPLICANT: Boyle, William J
; TITLE OF INVENTION: Fhm, A No. 685283931 Member of the TNF Ligand Supergene Family
; FILE REFERENCE: 0101/35550A
; CURRENT APPLICATION NUMBER: US/10/286,696
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/147,294
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin Ver. 2.0
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; SEQ ID NO 10
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Mouse
US-10-286-696-10

Qy   1 NAASIPSGSHKVTLSSWYHDRGWAKIS 27
          |||||||||||||||||||||||||||
Db   14 NAASIPSGSHKVTLSSWYHDRGWAKIS 40

Query Match   100.0%; Score 148; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 1.9e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
US-09-396-937-10
; Sequence 10, Application US/09396937
; Patent No. 6645500
; GENERAL INFORMATION:
; APPLICANT: M&E Biotech A/S
; APPLICANT: HALKIER, Torben
; APPLICANT: HAANING, Jesper
; TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
; FILE REFERENCE: 22021 PC 1
; CURRENT APPLICATION NUMBER: US/09/396,937
; CURRENT FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin Ver. 2.1
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; SEQ ID NO 10
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNA encoding
; OTHER INFORMATION: murine OPGL, residues 158-316, fused to His tag
US-09-396-937-10

Qy   1 NAASIPSGSHKVTLSSWYHDRGWAKIS 27
          |||||||||||||||||||||||||||
Db   27 NAASIPSGSHKVTLSSWYHDRGWAKIS 53

Query Match   100.0%; Score 148; DB 2; Length 173;
Best Local Similarity 100.0%; Pred. No. 5e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
US-09-396-937-12
; Sequence 12, Application US/09396937
; Patent No. 6645500
; GENERAL INFORMATION:
; APPLICANT: M&E Biotech A/S
; APPLICANT: HALKIER, Torben
; APPLICANT: HAANING, Jesper
; TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
; FILE REFERENCE: 22021 PC 1
; CURRENT APPLICATION NUMBER: US/09/396,937
; CURRENT FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 12
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion of
; OTHER INFORMATION: murine OPGL, residues 158-316 with C to S
; OTHER INFORMATION: mutation, and His tag
US-09-396-937-12

Qy   1 NAASIPSGSHKVTLSSWYHDRGWAKIS 27
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Db   27 NAASIPSGSHKVTLSSWYHDRGWAKIS 53

Query Match   100.0%; Score 148; DB 2; Length 173;
Best Local Similarity 100.0%; Pred. No. 5e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6
US-09-396-937-18
; Sequence 18, Application US/09396937
; Patent No. 6645500
; GENERAL INFORMATION:
; APPLICANT: M&E Biotech A/S
; APPLICANT: HALKIER, Torben
; APPLICANT: HAANING, Jesper
; TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
; FILE REFERENCE: 22021 PC 1
; CURRENT APPLICATION NUMBER: US/09/396,937
; CURRENT FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 18
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion between
; OTHER INFORMATION: murine OPGL, residues 158-316 with tetanus toxoid
; OTHER INFORMATION: P2 epitope introduced, and His tag
US-09-396-937-18

Qy   1 NAASIPSGSHKVTLSSWYHDRGWAKIS 27
          |||||||||||||||||||||||||||
Db   27 NAASIPSGSHKVTLSSWYHDRGWAKIS 53

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OM protein - protein search, using sw model

Run on: December 21, 2005, 13:02:07 ; Search time 14.8721 Seconds
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Title: US-09-211-297-32
Perfect score: 148
Sequence: 1 NAASIPSGSHKVTLSSWYHDRGWAKIS 27

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Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	148	100.0	27	5	US-10-825-898-33	Sequence 33, Appl
2	148	100.0	27	4	US-10-825-898-34	Sequence 34, Appl
3	148	100.0	77	4	US-10-286-696-10	Sequence 10, Appl
4	148	100.0	77	5	US-10-890-368-10	Sequence 10, Appl
5	148	100.0	77	5	US-10-889-948-10	Sequence 10, Appl
6	148	100.0	160	3	US-09-779-050A-14	Sequence 14, Appl
7	148	100.0	170	3	US-09-791-153A-76	Sequence 76, Appl
8	148	100.0	170	4	US-09-289-456-99	Sequence 99, Appl
9	148	100.0	173	4	US-10-664-801-10	Sequence 10, Appl
10	148	100.0	173	4	US-10-664-801-12	Sequence 12, Appl
11	148	100.0	173	4	US-10-664-801-18	Sequence 18, Appl
12	148	100.0	173	4	US-10-664-801-20	Sequence 20, Appl
13	148	100.0	182	4	US-10-664-801-16	Sequence 16, Appl
14	148	100.0	187	4	US-10-664-801-8	Sequence 8, Appl
15	148	100.0	188	4	US-10-664-801-14	Sequence 14, Appl
16	148	100.0	193	4	US-10-289-456-96	Sequence 96, Appl
17	148	100.0	199	4	US-10-050-902-224	Sequence 224, App
18	148	100.0	199	4	US-10-050-898-224	Sequence 224, Appl
19	148	100.0	199	4	US-10-289-456-86	Sequence 86, Appl
20	148	100.0	244	4	US-10-167-167-16	Sequence 16, Appl
21	148	100.0	244	4	US-10-460-623-16	Sequence 16, Appl
22	148	100.0	244	5	US-10-854-300-16	Sequence 16, Appl
23	148	100.0	244	4	US-11-135-521-16	Sequence 16, Appl
24	148	100.0	247	5	US-10-050-902-223	Sequence 223, App
25	148	100.0	247	4	US-10-050-898-223	Sequence 223, Appl
26	148	100.0	247	4	US-10-289-456-85	Sequence 85, Appl
27	148	100.0	249	4	US-10-338-785A-3	Sequence 3, Appli
28	148	100.0	249	4	US-10-611-363-3	Sequence 3, Appli
29	148	100.0	294	3	US-09-871-856-11	Sequence 11, Appl
30	148	100.0	294	3	US-09-865-363-11	Sequence 11, Appl
31	148	100.0	294	3	US-09-871-291-11	Sequence 11, Appl
32	148	100.0	294	3	US-09-877-650-11	Sequence 11, Appl
33	148	100.0	294	4	US-10-405-878-11	Sequence 11, Appl
34	148	100.0	294	5	US-10-802-133-11	Sequence 11, Appl
35	148	100.0	294	3	US-09-957-944-8	Sequence 8, Appl
36	148	100.0	316	3	US-09-079-569-7	Sequence 7, Appli
37	148	100.0	316	3	US-09-873-829-4	Sequence 4, Appli
38	148	100.0	316	3	US-09-933-915A-16	Sequence 16, Appli
39	148	100.0	316	4	US-10-017-910-4	Sequence 4, Appli
40	148	100.0	316	4	US-10-105-057-2	Sequence 2, Appli
41	148	100.0	316	4	US-10-272-411-19	Sequence 19, Appl
42	148	100.0	316	4	US-10-272-328A-19	Sequence 19, Appl
43	148	100.0	316	5	US-10-326-052-2	Sequence 2, Appli
44	148	100.0	316	4	US-10-167-182-1	Sequence 1, Appli
44	148	100.0	316	4	US-10-460-623-1	Sequence 1, Appli
45	148	100.0	316	4	US-10-338-785A-3	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-10-825-898-33

; Sequence 33, Application US/10825898
; Publication No. US2005003400A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS AND RECEPTORS
; FILE REFERENCE: A-451K REV 09-10-03 54SEQ
; CURRENT APPLICATION NUMBER: US/10/825,898
; CURRENT FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: US/10/825,898
; PRIOR FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: US 09/052,521
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: US 08/880,855
; PRIOR FILING DATE: 1997-06-23
; PRIOR APPLICATION NUMBER: US 08/842,842
; PRIOR FILING DATE: 1997-04-16
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 33
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-825-898-33

Query Match   100.0%; Score 148; DB 5; Length 27;
Best Local Similarity 100.0%; Pred. No. 6.8e-13;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 NAASIPSGSHKVTLSSWYHDRGWAKIS 27
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Db   1 NAASIPSGSHKVTLSSWYHDRGWAKIS 27

RESULT 2
US-10-825-898-34

; Sequence 34, Application US/10825898
; Publication No. US2005003400A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS AND RECEPTORS
; FILE REFERENCE: A-451K REV 09-10-03 54SEQ
; CURRENT APPLICATION NUMBER: US/10/825,898
; CURRENT FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: US/10/825,898
; PRIOR FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: US 09/052,521

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  PRIOR FILING DATE: 1998-03-30
  PRIOR APPLICATION NUMBER: US 08/880,855
  PRIOR FILING DATE: 1997-06-23
  PRIOR APPLICATION NUMBER: US 08/842,842
  PRIOR FILING DATE: 1997-04-16
  NUMBER OF SEQ ID NOS: 54
  SOFTWARE: Patentin version 3.1
  SEQ ID NO 34
  LENGTH: 28
  TYPE: PRT
  ORGANISM: Artificial Sequence
  FEATURE:
  OTHER INFORMATION: Synthetic Oligonucleotide
  US-10-825-898-34

Qy    1 NAASIPSGSHKVTLSSWYHDRGWAKIS 27
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Db    1 NAASIPSGSHKVTLSSWYHDRGWAKIS 27

Query Match           100.0%;
Best Local Similarity 100.0%;   Pred. No. 0;
Matches  27; Conservative  0; Mismatches  0; Indels  0; Gaps  0;
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RESULT 3
US-10-286-696-10
Sequence 10, Application US/10286696
Publication No. US20030129706A1
GENERAL INFORMATION:
  APPLICANT: Hsu, Hailing
  APPLICANT: Wooden, Scott K
  APPLICANT: Boyle, William J
  TITLE OF INVENTION: Fhm, A No. US20030129706A1e1 Member of the TNF Ligand Supergene F
  FILE REFERENCE: 01017/35550A
  CURRENT APPLICATION NUMBER: US/10/286,696
  CURRENT FILING DATE: 2002-11-01
  PRIOR APPLICATION NUMBER: US 10/286,696
  PRIOR FILING DATE: 1999-08-04
  NUMBER OF SEQ ID NOS: 22
  SOFTWARE: Patentin Ver. 2.0
  SEQ ID NO 10
  LENGTH: 77
  TYPE: PRT
  ORGANISM: Mouse
  US-10-286-696-10

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Query Match           100.0%;   Score 148;  DB 5;  Length 77;
Best Local Similarity 100.0%;   Pred. No. 7.1e-13;
Matches  27; Conservative  0; Mismatches  0; Indels  0; Gaps  0;

Qy    1 NAASIPSGSHKVTLSSWYHDRGWAKIS 27
        ||||||||||||||||||||||||||||
Db    1 NAASIPSGSHKVTLSSWYHDRGWAKIS 27
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RESULT 4
US-10-890-368-10
Sequence 10, Application US/10890368
Publication No. US20040248224A1
GENERAL INFORMATION:
  APPLICANT: Hsu et al.
  TITLE OF INVENTION: FHM, A NOVEL MEMBER OF THE TNF LIGAND SUPERGENE FAMILY: MATERIALS
  TITLE OF INVENTION: METHODS FOR INTERACTION MODULATORS
  FILE REFERENCE: 01017/35550D
  CURRENT APPLICATION NUMBER: US/10/890,368
  CURRENT FILING DATE: 2004-07-13
  PRIOR APPLICATION NUMBER: US 10/286,696
  PRIOR FILING DATE: 2002-11-01
  PRIOR APPLICATION NUMBER: US 09/632,287
  PRIOR FILING DATE: 2000-08-03
  PRIOR APPLICATION NUMBER: US 60/147,294
  PRIOR FILING DATE: 1999-08-04
  NUMBER OF SEQ ID NOS: 22

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Query Match           100.0%;   Score 148;  DB 5;  Length 77;
Best Local Similarity 100.0%;   Pred. No. 2e-12;
Matches  27; Conservative  0; Mismatches  0; Indels  0; Gaps  0;

Qy    1 NAASIPSGSHKVTLSSWYHDRGWAKIS 27
        ||||||||||||||||||||||||||||
Db   14 NAASIPSGSHKVTLSSWYHDRGWAKIS 40
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  SOFTWARE: Patentin Ver. 2.0
  SEQ ID NO 10
  LENGTH: 77
  TYPE: PRT
  ORGANISM: Mouse
  US-10-890-368-10
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RESULT 5
US-10-889-948-10
Sequence 10, Application US/10889948
Publication No. US20040265913A1
GENERAL INFORMATION:
  APPLICANT: Hsu et al.
  TITLE OF INVENTION: FHM, A NOVEL MEMBER OF THE TNF LIGAND SUPERGENE FAMILY: ANTIBODY
  TITLE OF INVENTION: MATERIALS AND METHODS
  FILE REFERENCE: 01017/35550C
  CURRENT APPLICATION NUMBER: US/10/889,948
  CURRENT FILING DATE: 2004-07-13
  PRIOR APPLICATION NUMBER: US 10/286,696
  PRIOR FILING DATE: 2002-11-01
  PRIOR APPLICATION NUMBER: US 09/632,287
  PRIOR FILING DATE: 2000-08-03
  PRIOR APPLICATION NUMBER: US 60/147,294
  PRIOR FILING DATE: 1999-08-04
  NUMBER OF SEQ ID NOS: 22
  SOFTWARE: Patentin Ver. 2.0
  SEQ ID NO 10
  LENGTH: 77
  TYPE: PRT
  ORGANISM: Mouse
  US-10-889-948-10

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Query Match           100.0%;   Score 148;  DB 5;  Length 77;
Best Local Similarity 100.0%;   Pred. No. 2e-12;
Matches  27; Conservative  0; Mismatches  0; Indels  0; Gaps  0;

Qy    1 NAASIPSGSHKVTLSSWYHDRGWAKIS 27
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Db   14 NAASIPSGSHKVTLSSWYHDRGWAKIS 40
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RESULT 6
US-09-779-050A-14
Sequence 14, Application US/09779050A
Patent No. US20020160416A1
GENERAL INFORMATION:
  APPLICANT: BOYLE, WILLIAM
  APPLICANT: HSU, HAILING
  TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
  FILE REFERENCE: A-570B
  CURRENT APPLICATION NUMBER: US/09/779,050A
  CURRENT FILING DATE: 2001-02-12
  PRIOR APPLICATION NUMBER: 60/181,800
  PRIOR FILING DATE: 2000-02-11
  NUMBER OF SEQ ID NOS: 52
  SOFTWARE: Patentin version 3.0
  SEQ ID NO 14
  LENGTH: 160
  TYPE: PRT
  ORGANISM: Mus musculus
  US-09-779-050A-14

Query Match   100.0%;   Score 148; DB 3; Length 160;
Best Local Similarity 100.0%;   Pred. No. 4.2e-12;
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OM protein - protein search, using sw model

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            GenCore version 5.1.6
            Copyright (c) 1993 - 2005 Compugen Ltd.

Run on:         December 21, 2005, 13:03:52 ; Search time 0.840984 Seconds
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Title:          US-09-211-297-32
Perfect score:  148
Sequence:       1 NAASIPSGSHKVTLSSWYHDRGWAKIS 27

Scoring table:  BLOSUM62
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Searched:       53982 seqs, 7132107 residues

Total number of hits satisfying chosen parameters:    53982

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	132	89.2	109	7	US-11-065-669-8	Sequence 8, Appli
2	53.5	36.1	1649	6	US-10-995-561-974	Sequence 974, App
3	53.5	36.1	1694	7	US-11-113-855-36	Sequence 36, Appl
4	53.5	36.1	1709	6	US-10-995-561-973	Sequence 973, App
5	53.5	36.1	1709	7	US-11-115-855-35	Sequence 35, Appl
6	46	31.1	532	7	US-11-152-747-2	Sequence 2, Appl
7	45	30.4	53	6	US-10-467-657-4496	Sequence 4496, Ap
8	44	29.7	401	6	US-10-467-657-810	Sequence 68, Appl
9	43.5	29.4	367	6	US-10-510-386-68	Sequence 1569, Ap
10	43.5	29.4	401	7	US-10-821-234-1569	Sequence 3, Appli
11	43.5	29.4	863	7	US-11-097-749-3	Sequence 2, Appli
12	43	29.1	245	6	US-10-793-626-2910	Sequence 2910, Ap
13	43	29.1	588	6	US-10-793-626-3328	Sequence 3328, Ap
14	42.5	28.7	447	7	US-11-112-882-4	Sequence 4, Appli
15	41	27.7	272	6	US-10-467-657-2730	Sequence 2730, Ap
16	41	27.7	288	6	US-10-131-826A-316	Sequence 316, App
17	41	27.7	987	6	US-10-770-726-61	Sequence 61, Appl
18	40.5	27.4	250	6	US-10-454-437-388	Sequence 388, App
19	40.5	27.4	378	7	US-11-080-091-3	Sequence 3, Appli
20	40.5	27.4	378	7	US-11-080-091-11	Sequence 11, Appl
21	40.5	27.4	378	7	US-11-087-177-39	Sequence 39, Appl
22	40.5	27.4	378	7	US-11-087-177-41	Sequence 41, Appl
23	40.5	27.4	488	7	US-10-821-234-1000	Sequence 1000, Ap
24	40	27.0	296	7	US-10-821-234-166	Sequence 166, App
25	40	27.0	362	6	US-10-821-234-1148	Sequence 1148, Ap
26	40	27.0	651	6	US-10-821-234-1480	Sequence 1480, Ap
27	40	27.0	2261	6	US-10-995-561-600	Sequence 600, App
28	40	27.0	2516	6	US-10-647-956A-2	Sequence 2, Appli
29	39.5	26.7	343	7	US-11-080-991-86	Sequence 86, Appl
30	39.5	26.7	393	6	US-10-821-234-1043	Sequence 1043, Ap
31	39	26.4	199	6	US-10-467-657-8058	Sequence 8058, Ap
32	39	26.4	261	6	US-10-617-034A-12	Sequence 12, Appl
33	39	26.4	282	7	US-10-467-657-810	Sequence 810, App
34	39	26.4	309	7	US-11-109-156-24	Sequence 24, Appl
35	39	26.4	309	7	US-11-109-156-39	Sequence 39, Appl
36	39	26.4	311	6	US-11-109-156-1638	Sequence 1638, Ap
37	39	26.4	322	6	US-10-821-234-1354	Sequence 1354, Ap
38	39	26.4	322	6	US-10-467-657-1638	Sequence 59, Appl
39	39	26.4	998	6	US-10-878-556A-59	Sequence 1, Appli
40	39	26.4	1467	6	US-10-821-234-1354	Sequence 59, Appl
41	38.5	26.0	366	7	US-11-091-334-9	Sequence 9, Appli
42	38.5	26.0	484	6	US-10-873-528-38	Sequence 38, Appl
43	38.5	26.0	617	6	US-10-878-556A-67	Sequence 67, Appl
44	38.5	26.0	659	6	US-10-467-657-6006	Sequence 6006, Ap
45	38	25.7	179	6	US-10-467-657-122	Sequence 122, App

ALIGNMENTS

RESULT 1
US-11-065-669-8
; Sequence 8, Application US/11065669
; Publication No. US2005024441A1
; GENERAL INFORMATION:
; APPLICANT: MacKay, Fabienne
; APPLICANT: Kalled, Susan
; TITLE OF INVENTION: BAFF, INHIBITORS THEREOF AND THEIR USE IN THE
; TITLE OF INVENTION: MODULATION OF B-CELL RESPONSE
; FILE REFERENCE: 08201.0024-04000
; CURRENT APPLICATION NUMBER: US/11/065,669
; CURRENT FILING DATE: 2005-02-24
; PRIOR APPLICATION NUMBER: 10/045,574
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 09/911,777
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/143,228
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: PCT/US00/01788
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/117,169
; PRIOR FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin Ver. 2.1
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; SEQ ID NO 8
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-065-669-8

Query Match   89.2%; Score 132; DB 7; Length 109;
Best Local Similarity   85.2%; Pred. No. 3.2e-12;
Matches   23; Conservative   1; Mismatches   3; Indels   0; Gaps   0;

Qy   1 NAASIPSGSHKVTLSSWYHDRGWAKIS 27
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Db   11 NATDIPSGSHKVSLSSWYHDRGWGKIS 37

RESULT 2
US-10-995-561-974
; Sequence 974, Application US/10995561
; Publication No. US2005027205A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
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; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 974
; LENGTH: 1649
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-974

Qy    3 ASIPSG------------SHKVTLSSWYHDRGW 23
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RESULT 3
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US-11-135-855-36
Sequence 36, Application US/11135855
Publication No. US20050255557A1
GENERAL INFORMATION:
APPLICANT: SMITHKLINE BEECHAM CORPORATION
APPLICANT: SMITHKLINE BEECHAM p.l.c.
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP50013
CURRENT APPLICATION NUMBER: US/11/135,855
CURRENT FILING DATE: 2005-05-24
PRIOR APPLICATION NUMBER: 60/182,172
PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: US/10/203,708
PRIOR FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: PCT/US01/04703
PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: 60/182,172
PRIOR FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: 60/186,084
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 36
LENGTH: 1694
TYPE: PRT
ORGANISM: Homo sapiens
US-11-135-855-36

Query Match    36.1%; Score 53.5; DB 7; Length 1694;
Best Local Similarity  31.2%;
Matches  10; Conservative  5; Mismatches  6; Indels  11; Gaps  1;

Qy    3 ASIPSG------------SHKVTLSSWYHDRGW 23
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Db 1263 AAVPEGAPITVTCADPAAHAPTLYTWHNGRW 1294
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RESULT 4
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US-10-995-561-973
Sequence 973, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 973
LENGTH: 1709
TYPE: PRT
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; ORGANISM: Homo sapiens
US-10-995-561-973

Query Match    36.1%; Score 53.5; DB 6; Length 1709;
Best Local Similarity  31.2%;
Matches  10; Conservative  5; Mismatches  6; Indels  11; Gaps  1;

Qy    3 ASIPSG------------SHKVTLSSWYHDRGW 23
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RESULT 5
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US-11-135-855-35
Sequence 35, Application US/11135855
Publication No. US20050255557A1
GENERAL INFORMATION:
APPLICANT: SMITHKLINE BEECHAM CORPORATION
APPLICANT: SMITHKLINE BEECHAM p.l.c.
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP50013
CURRENT APPLICATION NUMBER: US/11/135,855
CURRENT FILING DATE: 2005-05-24
PRIOR APPLICATION NUMBER: PCT/US01/04703
PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: 60/182,172
PRIOR FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: US/10/203,708
PRIOR FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: 60/186,084
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 35
LENGTH: 1709
TYPE: PRT
ORGANISM: Homo sapiens
US-11-135-855-35

Query Match    36.1%; Score 53.5; DB 7; Length 1709;
Best Local Similarity  31.2%;
Matches  10; Conservative  5; Mismatches  6; Indels  11; Gaps  1;

Qy    3 ASIPSG------------SHKVTLSSWYHDRGW 23
          |::|     |  |||::|
Db 1263 AAVPEGAPITVTCADPAAHAPTLYTWHNGRW 1294
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RESULT 6
```
US-11-152-747-2
Sequence 2, Application US/11152747
Publication No. US20050251881A1
GENERAL INFORMATION:
APPLICANT: E. I. du Pont de Nemours, Inc.
APPLICANT: Cheng, Qiong
APPLICANT: Tao, Luan
TITLE OF INVENTION: CAROTENOID KETOLASE GENE
FILE REFERENCE: CL-1849 US NA
CURRENT APPLICATION NUMBER: US/11/152,747
CURRENT FILING DATE: 2005-06-14
PRIOR APPLICATION NUMBER:
NUMBER OF SEQ ID NOS: 47
SOFTWARE: Microsoft Office 97
SEQ ID NO 2
LENGTH: 532
TYPE: PRT
ORGANISM: Rhodococcus erythropolis AN12
US-11-152-747-2

Query Match    31.1%; Score 46; DB 7; Length 532;
Best Local Similarity  39.3%;
Matches  11; Conservative  4; Mismatches  16; Indels  7; Gaps  2;
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